

Query Match	74.5%;	Score 1932;	DB 20;	Length 512;
Best Local Similarity	77.1%;	Pred. No. 2.1e-163;		
Matches	370;	Conservative 51;	Mismatches 51;	Indels 8; Gaps 4

  

Qy	14	VLPTQPLRLDHYLLGKLGQGGFTVYLCTEKTSTANVACKSIIPKRLKLVCREDEDVWR	73
Db	22	VLPORTQNIREVYVGRKLGGQGGFTTCTFRASGGKFAKSIIPKRLCKCEDIEDVWR	81
Qy	74	BIQIMHLLSEHPNVVRIKGTYESDVVFIHMEVCEGGELFDRIVSKGHSPSEAAVKLIKT	133
Db	82	BIQIMHLLSEHANVRIEGTYEDSTAVHLVMELCBGGELFDRIVKGHYSEKQAARLIKT	141
Qy	134	ILGVVEACHSIGVHWRDLKPNFLPDSPKDDAKLKATDFGLSVFYKPGQYLLDVVGSPPY	193
Db	142	IVEVVEACHSIGVHWRDLKPNFLPDTIDEDAKLKATDFGLSVFYKPGESFCDVVGSPPY	201
Qy	194	VAPEVLKKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLDFKSPDPWPTI	253
Db	202	VAPEVLRLKYGPESDVMSAGVILYLLSGVPPFWAESRPGIFRQILGKLDHFSEFWPSI	261
Qy	254	SEAKOLIIYKMLERSPKKRIISAHEALCHPIWIDVQAAFPKLPDPAVLGRKLFQFSQMNKIK	313
Db	262	SDSAKDLIRKWLQNPTRLTAHEVLRHPWIVDDNIAFDKPLDSAVLSRLKQFSAMNKLK	321
Qy	314	KMALRVIAERLSEBEIGGLKELFKMIDTDSGTITFEE----	369
Db	322	KMALRVIAERLSEBEIGGLKELFKMIDTDSGTITFDELKDLKDLKRVGSELMSESIK	381
Qy	370	SLMDAADIDNSGTIDYGEFLAATLHMKNKWEIEILVAAFPDKDQSGYITIDELQSACT	429
Db	382	DLMDAADIDKSGTIDYGEFIATVHLNKLREENLVSAFSDKQSGYITIDELQOACK	441
Qy	430	EFGLCDPLDMDWIKEDLDNKGKIDFSEFTAMRKGD--GVGRSRTMKNLNFNIADAFGV	488
Db	442	DFGLDDIHIDMDWIKEDQNDQIDYGEFAAMRKNGGIGCR-RTWRKTL--NLRDALGL	498

  

RESULT 6
AAG35778
ID AAG35778 standard; Protein; 399 AA.
XX AAG35778;
AC XX
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 43755.
DE Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX EF1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-0301439.
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 13-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 108 Seconds

(without alignments)  
1182.741 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPSPNTVLPTPT.....KNLNFNIADAFGVGDKSDD 495

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:.\*  
1: sp\_arChaea.\*  
2: sp\_bacteria.\*  
3: sp\_fungi.\*  
4: sp\_human.\*  
5: sp\_invertebrate.\*  
6: sp\_mammal.\*  
7: sp\_mhc.\*  
8: sp\_organelle.\*  
9: sp\_phage.\*  
10: sp\_plant.\*  
11: sp\_rodent.\*  
12: sp\_virus.\*  
13: sp\_vertibrate.\*  
14: sp\_unclassified.\*  
15: sp\_virus.\*  
16: sp\_bacteriap.\*  
17: sp\_arChaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	10	Q39016
2	2577	99.4	495	10	Q949P0
3	2458	97.8	557	10	Q9LQH7
4	2458	94.8	501	10	Q38869
5	2030	78.3	490	10	O24430
6	1969.5	76.0	496	10	Q93X19
7	1844.5	71.1	490	10	Q42396
8	1773	68.4	551	10	Q9FXQ3
9	1752	67.6	492	10	O04417
10	1751	67.5	487	10	Q43676
11	1746	67.3	558	10	Q8LPP8
12	1745	67.3	554	10	O04123
13	1742	67.2	556	10	Q38871
14	1739.5	67.1	578	10	Q93XJ0
15	1738	67.0	571	10	Q8LPP9
16	1733.5	66.9	578	10	Q93VF3

17	1731	66.8	544	10	Q38872
18	1728	66.6	581	10	Q93YF4
19	1719	66.3	646	10	Q38870
20	1717.5	66.2	578	10	O24460
21	1709.5	65.9	573	10	P3838
22	1709	65.9	483	10	Q39014
23	1708	65.9	581	10	Q93YF7
24	1700.5	65.6	484	10	Q9SZM3
25	1672.5	64.5	639	10	O82107
26	1671	64.4	565	10	Q8H544
27	1640.5	63.3	583	10	Q9ZV15
28	1630	62.9	451	10	Q41789
29	1592	61.4	542	10	Q9SNK9
30	1592	61.4	542	10	Q8GV21
31	1592	61.4	570	10	Q8H889
32	1587	61.2	542	10	O65003
33	1583	61.0	542	10	Q8H9A7
34	1531.5	59.1	548	10	Q9S724
35	1524.5	58.8	548	10	Q9S786
36	1509.5	58.2	528	10	Q8VYE7
37	1506.5	58.1	528	10	Q9FMP5
38	1484.5	57.3	540	10	O81390
39	1484	57.2	533	10	O81390
40	1482	57.2	531	10	Q94900
41	1482	57.2	531	10	Q9ZSA2
42	1480	57.1	518	10	Q9AXA7
43	1480	57.1	531	10	Q41790
44	1475	56.9	347	10	Q94IQ5
45	1473	56.8	553	10	Q8RW36

## ALIGNMENTS

RESULT 1

Q39016 PRELIMINARY; PRT; 495 AA.  
ID Q39016  
AC Q39016; (TREMREL. 01, Created)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)  
DE 01-MAR-2003 (TREMREL. 23, Last annotation update)  
DE Calcium-dependent protein kinase.  
GN ATCDPK2.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Columbia;  
RX MEDLINE=94359455; PubMed=8078458;  
RA Hayashida N., Shinozaki K.;  
RT "Two genes that encode Ca2+-dependent protein kinases are induced by drought and high-salt stresses in Arabidopsis thaliana.";  
RL Mol. Gen. Genet. 244:331-340(1994).  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL; D21806; BAA04830.1; -.  
DR HSSP; P02593; IFW4.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR007119; Prot\_kinase.  
DR Pfam; PF00036; ehand; 4.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000012; EF-hand; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00054; EFH; 4.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00018; EF\_HAND; 4.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.



DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE F1504.8.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RN [2]  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Ecker J.R.;  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao O., Johnson-Hopson C.,  
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,  
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,  
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N.,  
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,  
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,  
 RA Theologis A., Ecker J.;  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AC007887; AF479386.1; -;  
 DR HSP; P02593; IFW4.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr\_pkinase.  
 DR Pfam; PF00036; ehand; 4.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00054; EPH; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00018; EF HAND; 4.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 557 AA; 63397 MW; 7E92BA5A6B3A240B CRC64;  
  
 Query Match 97.8%; Score 2536; DB 10; Length 557;  
 Best Local Similarity 88.5%; Pred. No. 1.Se-182;  
 Matches 493; Conservative 0; Mismatches 2; Indels 62; Gaps 1;  
  
 QY 1 1 METKPNRPSNTVLPYQTPRLRDHYLLGKLGKGGQGTGYLCTEKSTSTANYACKSIPKR 60  
 DB 1 1 METKPNRPSNTVLPYQTPRLRDHYLLGKLGKGGQGTGYLCTEKSTSTANYACKSIPKR 60  
  
 QY 61 KLVCREDYEDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEYCEGELFDRIVSKG 120  
 DB 61 KLVCREDYEDVWREIQIMHLSHPNVVRKGYEDSVFVHIVMEYCEGELFDRIVSKG 120  
  
 QY 121 HFSERAVKLIKTLGVVACHSLGVNHRDLKPFNFDSPKDDAKLKATDFGLSVFYKP 180  
 DB 121 HFSERAVKLIKTLGVVACHSLGVNHRDLKPFNFDSPKDDAKLKATDFGLSVFYKP 180  
  
 QY 181 ----- 180  
 DB 181 GLIFLFWLDSLILQLVFWLVPVSMNRKLKQSGFLIETGLLFCFIWIANRNVGMVRFDD 240  
  
 QY 181 --GOYLVDVGGPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQI 238  
 DB 241 LFGQVLYDVGGPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQI 300  
  
 QY 239 LOGKLDKDPWPTTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPA 298  
 DB 301 LOGKLDKDPWPTTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPA 360  
  
 QY 299 VLRLKQFSQMNKIKMALRVIAERLSEEBIGGLKELFKWIDTNSGTTTFEELKAGLKR 358

## RESULT 4

Q38869 PRELIMINARY; PRT; 501 AA.  
 AC Q38869;  
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)  
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)  
 DE Calmodulin-domain protein kinase CDPK isoform 4 (fragment).  
 GN CPK4 OR T25922.10 OR AT4G09570.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RA McCombie W.R.;  
 RT "Arabidopsis thaliana Genomic Sequence, Chromosome IV. ";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA McCombie R.W., Spiegel L.A., Huang E.N., Nascimento L.U.,  
 RA de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R.,  
 RA O'Shaughnessy A., Rodriguez M., Shekher M., Schutz K., See L.H.,  
 RA Swaby I., Habermann K., Dedhia N.N., Mewes H.W., Lemcke K.,  
 RA Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M.,  
 RA Preston R.R., Matero A., Shah R., O'Shaughnessy A., Rodriguez M.,  
 RA Shekher M., Schutz K., See L.H., Swaby I., Habermann K., Dedhia N.N.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; U31752; AAB03243.1; -;  
 DR EMBL; AL161831; CAB8124.1; -;  
 DR EMBL; AL161515; CAB78080.1; -;  
 DR HSP; P02593; IFW4.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000719; Prot kinase.  
 DR InterPro; IPR002290; Ser Thr\_pkinase.  
 DR Pfam; PF00036; ehand; 4.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR ProDom; PD000001; Prot kinase; 1.  
 DR SMART; SM00054; EPH; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00018; EF HAND; 4.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 FT NON\_TER 1  
 SQ SEQUENCE 501 AA; 56416 MW; C709C17DFAF74B70 CRC64;



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Query Match          94.8%; Score 2458; DB 10; Length 501;
Best Local Similarity 94.8%; Pred. No. 9.3e-177;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KNPRLPNTVLPYQTPRLRDHYLGLGKLGQGFQGTYYLCTEKSTSNYACKSIIPKRLV 63
DB 3 KNPRLPNSVLPYETPRLDHYLGLGKLGQGFQGTYYLCTEKSSANYACKSIIPKRLV 62
QY 64 CREDYEDVWREIQIMHLSSEHPNVVRIKGTYESDSVFVHIVMEVCEGGLFDRIVSKGHFS 123
DB 63 CREDYEDVWREIQIMHLSSEHPNVVRIKGTYESDSVFVHIVMEVCEGGLFDRIVSKGCF 122
QY 124 EREAUKLTKTILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQY 183
DB 123 EREAUKLTKTILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQY 182
QY 184 LYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQLQGLK 243
DB 183 LYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQLQGLK 242
QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKLPDPAVL 303
DB 243 DFKSDPWPPTISEGAKDLIYKMLDRSPKKRIISAHEALCHPWIVDEHAAPDKLPDPAVL 302
QY 304 KQFSOMNKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSEL 363
DB 303 KQFSOMNKIKKMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSEL 362
QY 364 MESEIKSLMDAADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKDGGSGYITIDE 423
DB 363 MESEIKSLMDAADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKDGGSGYITIDE 422
QY 424 LQACTEFGCLDTPLDMMIKKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIA 483
DB 423 LQACTEFGCLDTPLDMMIKKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIA 482
QY 484 DAFGVG---EKSDD 495
DB 483 EAFGVEDTSSTAKSDD 498

RESULT 5
O24430 PRELIMINARY; PRT; 490 AA.
AC O24430;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calmodulin-like domain protein kinase isoenzyme beta.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RN SEQUENCE FROM N.A.
RP McKendree W.L., Doostdar H., McCallum T.G., Mayer R.T.;
RT "cDNA cloning and expression of a gene (Accession No. Z97064) from
RT Citrus paradisi roots similar to bacterial YRN1 and HEAH10 proteins
RT and an mRNA from Brassica oleracea that is wound and dark inducible
RT (PGR97-127).";
RL Plant Physiol. 115:314-314(1997).
RN [2]
RN SEQUENCE FROM N.A.
RP Lee J.-Y., Yoo B.-C., Harmon A.C.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; U69173; AAB80692.1; -.
DR HSP; P02588; 1PON
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; efhnd; 4.
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Pfam; PF00069; pkinase; 1.
DR ProDom; PD000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; EFh; 4.
DR SMART; SM00054; EFh; 4.
DR PROSITE; PS00018; EF HAND; 4.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 490 AA; 55164 MW; 2333C411CAA43E0F CRC64;

Query Match          78.3%; Score 2030; DB 10; Length 490;
Best Local Similarity 81.1%; Pred. No. 1.6e-144;
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;

QY 14 VLPQTPLRLDHYLGLGKLGQGFQGTYYLCTEKSTSNYACKSIIPKRLVCREYEDVWR 73
DB 12 VLPQTPLRLDHYLGLGKLGQGFQGTYYLCTEKSTSNYACKSIIPKRLVCREYEDVWR 71
QY 74 EIQIMHLSSEHPNVVRIKGTYESDSVFVHIVMEVCEGGLFDRIVSKGHFSREAVKLTK 133
DB 72 EIQIMHLSSEHPNVVRIKGTYESDSVFVHIVMEVCEGGLFDRIVSKGHFSREAVKLTK 131
QY 134 ILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY 193
DB 132 ILGVVEACHSLGVMRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPYY 191
QY 194 VAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQLQGLKDFKSDPWPPT 253
DB 192 VAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQLQGLKDFKSDPWPPT 251
QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKLPDPAVLRLKQFSOMNKIK 313
DB 252 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKLPDPAVLRLKQFSOMNKIK 310
QY 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSEIKSLMD 373
DB 311 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSEIKSLMD 370
QY 374 AADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKDGGSGYITIDELOQACKPFL 433
DB 371 AADINDSGTIDYGEFLAATLHMNMEREELVAAFSDFDKDGGSGYITIDELOQACKPFL 430
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIAADAFGM 488
DB 431 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMKNLNFNIAADAFGM 486

RESULT 6
Q93X19 PRELIMINARY; PRT; 496 AA.
AC Q93X19;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium dependent protein kinase.
GN RICDPK2.
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. Rishiri;
RC Furuichi N., Okuta T., Hara N.;
RT "Calcium dependent protein kinase genes from resistant and susceptible
RT potato cultivars to Phytophthora infestans";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB051809; BAB63464.1; -.
DR InterPro; IPR002048; EF-hand.
```



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RESULT 8
Q9FXQ3 ID Q9FXQ3 PRELIMINARY; PRT; 551 AA.
AC Q9FXQ3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE OsCDPK7.
GN OSCDPK7.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=20387027; PubMed=10929125;
RA Saijo Y., Hata S., Kozuka J., Shimamoto K., Izui K.;
RT "Over-expression of a single Ca2+-dependent protein kinase confers
RT both cold and salt/drought tolerance on rice plants.";
RL Plant J. 23:319-327(2000).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AB042550; BAB16888.1; -.
DR HSSP; P02593; ICTR.
DR Gramene; Q9FXQ3; -.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD0000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; Eph; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 551 AA; 60966 MW; E479A089EF287A7B CRC64;

Query Match 68.4%; Score 1773; DB 10; Length 551;
Best Local Similarity 71.2%; Pred. No. 4.5e-125;
Matches 339; Conservative 53; Mismatches 82; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGTTLCTEKTSTANYACKSIPKRLVCREDYEDVW 72
DB 75 SVLGHTPNLRDLVAMGRKLGQGGTTLCTELSTGVVDYACKSISKRLITKEDVDV 134
QY 73 REIQIMHLSHPNVVRIKGTYESVVFHIVMEVCEGGLFDRIVSKGHFSEREAVKLK 132
DB 135 REIQIMHLSGHKNVVAIKGAYEDQVYVHIVMELCAGELFDRIIQRGHYSERKAAELTR 194
QY 133 TILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKQVLYDVVGSYP 192
DB 195 IIVGVVEACHSLGVNHRDLKPNFLFANLANKDDLSLKATDFGLSVFYKQVLYDVVGSYP 254
QY 193 YVAPVLKCKVGPETDVMSAGVILYLLSGVPPFMAETSGIFRQILQGLKDFKSDPWP 252
DB 255 YVAPVLKCKVGPEDAVMTAGVILYLLSGVPPFMAETQOGIFDFAVLKGFIDFSDPWP 314
QY 253 ISEAADLIYKMLERSPKKRISAEALCHPMIVDEQAAPDKPLDPAVLSRLKQFSOMNKK 312
DB 315 ISEAKOLITKMLNRPKRLTAHEVLCHPMIRDHGVPADPLDPAVLSRLKQFSOMNKK 374
QY 313 KKMALRVIAELSBEEIGGLKELFMIDTNSGTTTPEELKAGLRVGSSELSSEIKSLM 372
DB 375 KKMALRVIAELSBEEITAGLEMFTQMDADNSGAIITYDELKGLRKYGSTLKTDEIRDL 434
QY 373 DAADIDNSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFG 432

Db 435 DAADIDNSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFG 494
QY 433 LCDTPLDDMIKIDLDNGKIDFSEFTAMRRKGD-GVGRSRTMMKNLNFNIADAFG 487
DB 495 MFDAFLDDVINEADQNDGRIDYGEFVAMTKGNMGVGR-RTMRNSLNISMRDAPG 549

RESULT 9
O04417 ID O04417 PRELIMINARY; PRT; 492 AA.
AC O04417;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Calcium dependent protein kinase.
GN ZMCDPK1.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=honey bantum;
RA Berberich T., Kusano T.;
RT "Cycloheximide induces a subset of low-temperature-inducible genes in
RT maize.";
RL Mol. Gen. Genet. 0:0-0(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97294505; PubMed=9150261;
RA Berberich T., Kusano T.;
RT "Cycloheximide induces a subset of low temperature-inducible genes in
RT maize.";
RL Mol. Gen. Genet. 254:275-283(1997).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; D84408; BAA12338.1; -.
DR HSSP; P02593; ICTR.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00036; ehand; 4.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD0000012; EF-hand; 2.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00054; Eph; 4.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00018; EF_HAND; 4.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 492 AA; 54734 MW; 8615C3C3606CE949 CRC64;

Query Match 67.6%; Score 1752; DB 10; Length 492;
Best Local Similarity 70.6%; Pred. No. 1.5e-123;
Matches 334; Conservative 54; Mismatches 83; Indels 2; Gaps 2;

QY 13 TVLPYQTPRLRDHYLLGKLGQGGTTLCTEKTSTANYACKSIPKRLVCREDYEDVW 72
DB 14 SVLGHTPNLRDLVAMGRKLGQGGTTLCTELSTGVVDYACKSISKRLITKEDVDV 73
QY 73 REIQIMHLSHPNVVRIKGTYESVVFHIVMEVCEGGLFDRIVSKGHFSEREAVKLK 132
DB 74 REIQIMHLSGHKNVVAIKGAYEDQVYVHIVMELCAGELFDRIIQRGHYSERKAAELTR 133
QY 133 TILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKQVLYDVVGSYP 192
DB 134 IIVGVVEACHSLGVNHRDLKPNFLFANLANKDDLSLKATDFGLSVFYKQVLYDVVGSYP 193
QY 193 YVAPVLKCKVGPEDVMSAGVILYLLSGVPPFMAETSGIFRQILQGLKDFKSDPWP 252
```

Db 194 YVAPEVLKSYGPAADVWTVAGVILYLLSGVPPFAETQOGIFDAVLKGAIDFSDPWPV 253  
QY 253 ISEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQWNKI 312  
Db 254 ISDSAKDLIRMLNPRPAERLTAHEVLCHPWIRDHGVAPDRPLDPAVLSRIKQFSANVKL 313  
QY 313 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLM 372  
Db 314 KQALRVIAERLSEEEIAGLKEMFQMTDNTNSGTTTFEELKAGLRKRVGSELMESEIKSLM 373  
QY 373 DAADIDNSGTTIDYGEFLAATLHNMKMEREEILVAASDFDKDGGSYITIDELQSACTEFG 432  
Db 374 DAADIDNSGTTIDYGEFLAATLHNMKMEREEILVAASDFDKDGGSYITIDELQSACTEFG 433  
QY 433 LCTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 484  
Db 434 MPDAFLDDVINEADQDNDGRIDYGEFVAMMTKGNMGVGR-RTMRSNLINISMRD 485

## RESULT 10

Q43676 PRELIMINARY; PRT; 487 AA.  
AC Q43676;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Calcium dependent protein kinase.  
GN CDPK.  
OS Phaseolus aureus (Mung bean) (Vigna radiata).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Vigna.  
OX NCBI\_TaxId=3916;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=wilcz, and cv. Berken; TISSUE=Etisolated hypocotyl;  
RX MEDLINE=96311003; PubMed=8704124; Villa M., Arteca R.N.;  
RA Botella J.R., Arteca J.M., Somodevilla M., Arteca R.N.;  
RT "Calcium-dependent protein kinase gene expression in response to  
physical and chemical stimuli in mungbean (Vigna radiata).";  
RL Plant Mol. Biol. 30:1129-1137(1996).  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR HSSP; Q63450; 1A06.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00036; ehand; 4.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00054; EPH; 4.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00018; EF\_HAND; 4.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 487 AA; 54700 MW; 54E6FBF5D93AEB2 CRC64;

Query Match 67.5%; Score 1751; DB 10; Length 487;  
Best Local Similarity 69.1%; Pred. No. 1.7e-123;  
Matches 327; Conservative 64; Mismatches 80; Indels 2; Gaps 2;

QY 14 VLPTQTPRLRDHYLLGKLGQGGFGTTTLCTEKSTSANVACKSIKPKLVCKREDVEDVWR 73  
Db 12 VLGHKTPNIRDLYTLGRKLGGQGGFGTTTLCTENSTSNVACKSIKPKLVCKREDVEDVWR 71  
QY 74 ELQIMHHLSEHNVRVRIKTYEDSVFVHIVMEVCGGELFDRIVSKGHFSERAEVLIKT 133  
Db 72 ELQIMHHLAGHKNIVITKAGVEDPLYVHIVMELCSGGELFDRIQGHVTERKAAELTKI 131

QY 134 ILGVWBAHSLGVHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
Db 132 IVGWEACHSLGVHRLDKPENFLVKNKDDFSLKAIDFGLSVFFKPGQIFTDVVGSPY 191  
QY 194 VAPEVLKCYGPRIDVNSAGVILYLLSGVPPFAETESGIFQIOLGKLDKDFSDPPTI 253  
Db 192 VAPEVLKHYGPADVWTVAGVILYLLSGVPPFAETQOGIFDAVLKGHIDFSDPWPVLI 251  
QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQWNKI 313  
Db 252 SDGSKDLIRMLCSQPSERLTAHVLCWPICENGVAPOAIDPAVLRLKQFSAMNKLK 311  
QY 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELMESEIKSLMD 373  
Db 312 KQALRVIAERLSEEEIAGLRKEMFQMTDNTNSGTTTFEELKAGLRKRVGSELMESEIKSLMD 371  
QY 374 ADIDNSGTTIDYGEFLAATLHNMKMEREEILVAASDFDKDGGSYITIDELQSACTEFG 433  
Db 372 AADVDSGTTIDYGEFLAATLHNMKMEREEILVAASDFDKDGGSYITIDELQSACTEFG 431  
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD 485  
Db 432 TDAFLDIIREVDDNDGRIDYGEFAAMMQKNAGIGR-RTMRSNLINISMRDA 483

## RESULT 11

Q8LPV8 PRELIMINARY; PRT; 558 AA.  
AC Q8LPV8;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Calmodulin-like domain protein kinase CPK2.  
OC Cucurbita maxima (Pumpkin) (Winter squash).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid1; Cucurbitales; Cucurbitaceae; Cucurbita.  
OX NCBI\_TaxId=3661;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=cv. Big Max;  
RX MEDLINE=21975187; PubMed=11847230;  
RA Yoo B.C., Lee J.Y., Lucas W.J.;  
RT "Analysis of the Complexity of Protein Kinases within the Phloem Sieve  
Tube System. CHARACTERIZATION OF CUCURBITA MAXIMA CALMODULIN-LIKE  
DOMAIN PROTEIN KINASE 1.";  
RL J. Biol. Chem. 277:15325-15332(2002).  
DR EMBL; AY072802; AAL68972.1; --  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR001245; Tyr\_pkinase.  
DR Pfam; PF00036; ehand; 4.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR ProDom; PD000012; EF-hand; 2.  
DR SMART; SM00054; EPH; 4.  
DR SMART; SM00220; S\_TKC; 1.  
DR SMART; SM00219; TyrKc; 1.  
DR PROSITE; PS00018; EF\_HAND; 4.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 558 AA; 62526 MW; 4D62EB5D74F516B CRC64;

Query Match 67.3%; Score 1746; DB 10; Length 558;  
Best Local Similarity 69.5%; Pred. No. 5e-123;  
Matches 330; Conservative 59; Mismatches 84; Indels 2; Gaps 2;

QY 14 VLPTQTPRLRDHYLLGKLGQGGFGTTTLCTEKSTSANVACKSIKPKLVCKREDVEDVWR 73  
Db 83 VLGHKTPNIRDLYTLGRKLGGQGGFGTTTLCTEIMTGIEYACKSIKPKLVCKREDVEDVRR 142

Qy 74 EIQMHLSHPNVVRKGTIEDSVFVHMEVCEGGELFDRIVSKGHFSREAVKLIK 133  
 Db 143 EIQMHLSHPNVVRKGTIEDSVFVHMEVCEGGELFDRIVSKGHFSREAVKLIK 202  
 Qy 134 ILGVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPY 193  
 Db 203 ILGVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPY 262  
 Qy 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFAETESGIFRILQGLKDFKSDPWTI 253  
 Db 263 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFAETESGIFRILQGLKDFKSDPWTI 322  
 Qy 254 SEAAKDLIYKMLERSPKKRISAEHALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKK 313  
 Db 323 SDSAKDLIRRMCLSPRSDRLTAHEVLCHPWIRWDHGVAPDRPLDPAVLSRLKQFSOMNKK 382  
 Qy 314 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 373  
 Db 383 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 442  
 Qy 374 AADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGSYITIDELQSACTEFG 433  
 Db 443 AADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGSYITIDELQSACTEFG 502  
 Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMMKNLNFNIADAFG 487  
 Db 503 TDAYLEIIRVDQNDGRIDYSEFVAMMOKGNAGIGR-RTMRNSLNSMRDGP 556

## RESULT 12

O04123 ID O04123 PRELIMINARY; PRT; 554 AA.  
 AC O04123;  
 DT 01-JUL-1997 (TrEMBLrel. 04, Created)  
 DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Calcium-dependent protein kinase.  
 OS Zea mays (Maize).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 OX NCBI\_TaxID=4577;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=inbred line H84;  
 RX MEDLINE=97201047; PubMed=9048876;  
 RA Saijo Y., Hata S., Sheen J., Izui K.;  
 RT "cDNA cloning and prokaryotic expression of a maize calcium-dependent  
 protein kinase".  
 RL Biochim. Biophys. Acta 1350:109-114(1997).  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; D87042; BAA13232.1; -;  
 DR HSSP; P02593; 1CTR.  
 DR InterPro; IPR002048; EF-hand.  
 DR InterPro; IPR000719; Prot\_kinase.  
 DR InterPro; IPR002290; Ser\_Thr\_pkinase.  
 DR Pfam; PF00036; ehand; 4.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000012; EF-hand; 2.  
 DR ProDom; PD000001; Prot\_kinase; 1.  
 DR SMART; SM00054; EFh; 4.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00018; EF\_HAND; 4.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 554 AA; 61056 MW; 51FC6F44684C57C6 CRC64;

Query Match 67.3%; Score 1745; DB 10; Length 554;  
 Best Local Similarity 70.0%; Pred. No. 5.9e-123;  
 Matches 333; Conservative 57; Mismatches 84; Indels 2; Gaps 2;

Qy 13 TVLPYOTPLRDHYLLGKLGOGQGTTLCTEKSSTANYACKSIKKKLVCREDEYDVM 72  
 Db 78 SVLGHTPNURDLVALGRKLGOGQGTTLCTEATGVDYACKSISKKKLTITREDDVDR 137  
 Qy 73 REIQMHLSHPNVVRKGTIEDSVFVHMEVCEGGELFDRIVSKGHFSREAVKLIK 132  
 Db 138 REIQMHLSHPNVVRKGTIEDSVFVHMEVCEGGELFDRIVSKGHFSREAVKLIK 197  
 Qy 133 TIIGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPY 192  
 Db 198 TIIGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPY 257  
 Qy 193 YVAPVLLKCYGPEIDVMSAGVILYLLSGVPPFAETESGIFRILQGLKDFKSDPWTI 252  
 Db 258 YVAPVLLKCYGPEIDVMSAGVILYLLSGVPPFAETESGIFRILQGLKDFKSDPWTI 317  
 Qy 253 ISAAKDLIYKMLERSPKKRISAEHALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKK 312  
 Db 318 ISDSAKDLIRRMCLSPRSDRLTAHEVLCHPWIRWDHGVAPDRPLDPAVLSRLKQFSOMNKK 377  
 Qy 313 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 372  
 Db 378 KQALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRVGSSELMSEIKSLMD 437  
 Qy 373 DAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGSYITIDELQSACTEFG 432  
 Db 438 DAADIDNSGTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGSYITIDELQSACTEFG 497  
 Qy 433 LCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRRTMMKNLNFNIADAFG 487  
 Db 498 MPDAFLDDVINEADQNDGRIDYGEFVAMMOKGNAGIGR-RTMRNSLNSMRDGP 552

RESULT 13  
 Q38871 ID Q38871 PRELIMINARY; PRT; 556 AA.  
 AC Q38871;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
 DE Calmodulin-domain protein kinase CDPK isoform 5.  
 GN CPK5 OR F23B12.130 OR AT4G35310.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=COLUMBIA;  
 RA Hrabak E.M., Dickmann L.J., Satterlee J.S., Sussman M.R.;  
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Bevan M., Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,  
 RA Hoheisel J., Jesse T., Heijnen L., Vos P., Mewes H.W., Mayer K.F.X.,  
 RA Schueller C.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Hilbert H., Braun M., Holzer E., Brandt A., Duesterhoeft A.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; U31834; AAB03245.1; -;  
 DR EMBL; AL022604; CAA18738.1; -;  
 DR EMBL; AL161587; CAB80248.1; -;  
 DR HSSP; P02588; 1TNX.

DR	InterPro; IPR002048; EF-hand.	RC	STRAIN=ev. Rishiri;
DR	InterPro; IPR000719; Prot_kinase.	RA	Furuichi N., Okuta T., Hara N.;
DR	InterPro; IPR002290; Ser_thr_kinase.	RT	"Calcium dependent protein kinase genes from resistant and susceptible
DR	Pfam; PF00036; ehand; 4.	RL	potato cultivars to Phytophthora infestans.";
DR	Pfam; PF00069; pkinase; 1.	RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR	ProDom; PD000012; EF-hand; 2.	CC	-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR	ProDom; PD000001; Prot_kinase; 1.	DR	EMBL; AB051808; BAB63463.1; -.
DR	SMART; SM00054; Efh; 4.	DR	InterPro; IPR002048; EF-hand.
DR	SMART; SM00220; S_TKc; 1.	DR	InterPro; IPR000719; Prot_kinase.
DR	PROSITE; PS00018; EF_HAND; 4.	DR	InterPro; IPR002290; Ser_thr_kinase.
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	DR	Pfam; PF00036; ehand; 4.
DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.	DR	Pfam; PF00069; pkinase; 1.
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	DR	ProDom; PD000012; EF-hand; 2.
KW	ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.	DR	ProDom; PD000001; Prot_kinase; 1.
SQ	SEQUENCE 556 AA; 62127 MW; 737F1ADD582B45ED CRC64;	DR	SMART; SM00054; Efh; 4.
Query Match 67.2%; Score 1742; DB 10; Length 556;		DR	SMART; SM00220; S_TKc; 1.
Best Local Similarity 68.4%; Pred. No. 1e-122;		DR	PROSITE; PS00018; EF_HAND; 4.
Matches 329; Conservative 66; Mismatches 84; Indels 2; Gaps 2;		DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
QY	6 NRRPSNTVLPVQTPRLRDHYLLGKLGQGGTGYLCTEKSTSYACKSIPKRKLVCYR 65	DR	PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DB	77 NPDNQAYVYVGHKTNIRDIYTLRSKLGQGGTGYLCTEIASGVVDYACKSISKRLISK 136	DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
QY	66 EDYEDVWREIQIMHLSHPNVVRIKGYEDSVFVHIVMEVCEGGLFDRIIVSKGHPSEYR 125	KW	ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
DB	137 EDVEDVRRREIQIMHLAGSGSVITIKGAYEDSLYHIVNELCAGGELFDRIIQRGHYSER 196	SQ	SEQUENCE 556 AA; 62127 MW; 737F1ADD582B45ED CRC64;
QY	126 EAVKLITKILGVVEACHSLGVNHRDLKPNFLLFDSPKDDAKLKATDFGLSVFYPKQGYLY 185	Query Match 67.1%; Score 1739.5; DB 10; Length 578;	
DB	197 KAAELTKIIVGVVEACHSLGVNHRDLKPNFLLVKNKDDDFSLKATDFGLSVFYPKQGYLY 256	Best Local Similarity 67.6%; Pred. No. 1.6e-122;	
QY	186 DVVSGPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDF 245	Matches 326; Conservative 62; Mismatches 79; Indels 15; Gaps 1;	
DB	257 DVVSGPYVVAPEVLKRYGPEADVMTAGVILYLLSGVPPFWAETQGGIFDAVLKGYIDF 316	QY	2 ETKNPRRP-----SNTVLPYQTPRLRDHYLLGKLGQGGTGYLCTEK 46
QY	246 KSDPWTISEAAKLIYKMLERSPKKRISEAELCHPWIVDEQAAPDKPLPAVLRLKQ 305	DB	75 EEQPPKPKPKPAEKWRVSSAGLRKTDVQLKKTGNLKEFFSIGRKLGGQGGTTFKCEVK 134
DB	317 ESDPWPVLSDSAKLIIRMLSKPAERLTAHEVLRHPWICENGVAAPDRAALDPAVLRLKQ 376	QY	47 STSANYACKSIPKRKLVCREDYEDVWREIQIMHLSHPNVVRIKGYEDSVFVHIVMEV 106
QY	306 FSQMKIKKMLRVIAERLSBEEIIGGLKELFKMIDTNSGTTTFPEELKAGLRKVGSELME 365	DB	135 ATGKEYACKSIAKRKLKLTDDDDVEDVRREVQIMHLAGHPHVISIKGAYEDAVAHVMEF 194
DB	377 FSAMNKKKMLKVIAESLSSEEEIAGLRQEMFQAMDTNSGALTDFELKAGLRKYGSTLKD 436	QY	107 CEGGELFDRIIVSKGHFSEREAVALIKITILGVVEACHSLGVNHRDLKPNFLLFDSPKDDAK 166
QY	366 SEIKSLMDAADTNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGSYITIDELQ 425	DB	195 CAGGELFDRIIQRGHYTERKAAELTRITGVVEACHSLGVNHRDLKPNFLLFVQDKEDSL 254
DB	437 TEIHLMDAADVNSGTTIDYSEFTAATLHNLKEREHLVAFAFQFDKDGSGFTIDELQ 496	QY	167 LKATDFGLSVFYPKQGYLYDVVSGPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPF 226
QY	426 SACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GYGRSRMTMMKNLNFNIAD 484	DB	255 LKATDFGLSVIFPKPGDFTDVVSGPYVVAPEVLKRYGPEADVMSAGVILYLLSGVPPF 314
DB	497 QACVEHGNADVLEDTIIEVDNDNDGKIDYGEFVEMMQGNAGVR-RTMRNSLNISMRD 555	QY	227 WAETESGIFRQILQGLKDFKSDPWTISEAAKLIYKMLERSPKKRISEAELCHPWIVD 286
QY	485 A 485	DB	315 WAENQEGIFEQVLHGLDLDKSDPWSISEDAKLMRMLVDRPRLRLTAHEVLCHPNVQV 374
DB	556 A 556	QY	287 EQAAPDKPLDPAVLRLSKQFSQMNKIKKMLRVIAERLSBEEIIGGLKELFKMIDTNSGT 346
RESULT 14		DB	375 DGVAPDKPLDSAVLSRMKQFSAMNKKKMLRVIAESLSSEEEIAGLKEMFKMIDTNSGQ 434
Q93XJ0	PRELIMINARY; PRT; 578 AA.	QY	347 ITPEELKAGLRKVGSELMESEIKSLMDAADTNSGTTIDYGEFLAATLHMNMKEREELVA 406
AC	Q93XJ0;	DB	435 ITPEELKAGLRKFGSNLKETEIYDLMDAADVNSGTTIDYGEFIAATLHMNKIERQDHLFA 494
DT	01-DEC-2001 (TrEMBLrel. 19, Created)	QY	407 AFSDFDKDGSGYITIDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD 466
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)	DB	495 AFCYFDKDGSGYITADELQACEFGIGDVRMEEMIREADQDNDGRIIDYNEFVAMMQGN 554
DE	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	QY	467 GV 468
DE	Calcium dependent protein kinase.	DB	555 PV 556
GN	RICDPK1.	RESULT 15	
OS	Solanum tuberosum (Potato).	Q8LPV9	PRELIMINARY; PRT; 571 AA.
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	ID	Q8LPV9
OC	Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;	AC	Q8LPV9;
OC	Asteridae; Lamiales; Solanales; Solanaceae; Solanum.	DT	01-OCT-2002 (TrEMBLrel. 22, Created)
OX	NCBI_TaxID=4113;	DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
RN	[1]	DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
RP	SEQUENCE FROM N.A.	DE	Phloem calmodulin-like-domain protein kinase PCPK1.
RP		OS	Cucurbita maxima (Pumpkin) (Winter squash).



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 81 Seconds  
(without alignments)  
969.996 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPNTVLPYQTP.....KNLNFNTADAFVGDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2593	100.0	495	23	AA048000
2	2458	94.8	501	21	AA035776
3	2458	94.8	501	23	AA048001
4	2064	79.6	425	21	AA035777
5	1932	74.5	512	20	AA093256
6	1924	74.2	399	21	AA035778
7	1742	67.2	483	21	AA031158
8	1742	67.2	556	21	AA031157
9	1703	65.7	856	21	AA038599

10	1703	65.7	893	21	AA038598
11	1703	65.7	1017	21	AA038597
12	1672.5	64.5	639	23	ABP53637
13	1509.5	58.2	549	23	AA052842
14	1509	58.2	408	21	AA031159
15	1501	57.9	463	21	AA046565
16	1500	57.8	280	22	AA065758
17	1462	56.4	529	21	AA029590
18	1462	56.4	542	21	AA029589
19	1460.5	56.3	459	21	AA029591
20	1457	56.2	569	15	AA056237
21	1325.5	51.1	538	21	AA043621
22	1319	50.9	404	21	AA046566
23	1231	47.5	378	21	AA046567
24	1187.5	45.8	307	20	AA093255
25	1166.5	45.0	424	21	AA043622
26	1153.5	44.5	421	21	AA043623
27	1059	40.8	413	22	AA065755
28	1015.5	39.2	523	21	AA010101
29	928.5	35.8	426	21	AA010102
30	920.5	35.5	302	21	AA054428
31	900	34.7	274	22	AA065756
32	887	34.2	274	19	AA049837
33	887	34.2	274	22	AA065757
34	887	34.2	274	22	AA065759
35	849	32.7	597	23	AA052841
36	842.5	32.5	384	21	AA010103
37	829	32.0	623	22	AA055583
38	829	32.0	623	23	ABP53630
39	826	31.9	625	23	ABP53638
40	800	30.9	576	23	ABP53639
41	771.5	29.8	456	16	AA074996
42	753.5	29.1	504	21	AA016593
43	753.5	29.1	594	21	AA016592
44	737	28.4	502	21	AA033884
45	737	28.4	594	21	AA053883

#### ALIGNMENTS

#### RESULT 1

AA048000  
ID AA048000 standard; Protein; 495 AA.

XX AA048000;

XX AC

XX DT 08-MAR-2002 (first entry)

XX DE

XX KW Arabidopsis CDPK2 SEQ ID NO 1.

XX KW Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;

XX KW disease resistance; agricultural; pathogen; crop yield; ornamental;

XX KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;

XX KW transgenic; plant; enzyme.

XX OS Arabidopsis thaliana.

XX PN WO200184911-A1.

XX PD 15-NOV-2001.

XX PF 04-MAY-2001; 2001WO-US14368.

XX PR 05-MAY-2000; 2000US-201925P.

XX PA (GENO ) GEN HOSPITAL CORP.

XX PI Sheen J;

XX PI WPI; 2002-062179/08.

XX DR N-PSDB; ABA06021.

XX DR



PT Producing plant having increased disease resistance, comprises  
PT regenerating plant from a non-naturally occurring plant cell  
PT over-expressing a polynucleotide encoding a calcium dependent protein  
XX kinase polypeptide  
XX  
XX Disclosure; Fig 1; 44pp; English.  
XX  
CC The invention relates to producing a plant having increased disease  
CC resistance, comprising providing a non-naturally occurring plant cell  
CC over-expressing a polynucleotide encoding a calcium dependent protein  
CC kinase (CDPK) polypeptide and regenerating a plant from the plant  
CC cell, where the CDPK polypeptide is expressed in the plant, increasing  
CC the resistance of the plant to disease as compared to a  
CC naturally-occurring plant. The method is useful for a variety of  
CC agricultural and commercial purposes including improving a plant's  
CC resistance against plant pathogens, increasing crop yields, improving  
CC crop and ornamental quality and reducing agricultural production costs.  
CC The method facilitates an effective and economical method for in-plant  
CC protection against plant pathogen, reducing or minimising the need for  
CC traditional chemical practices (e.g. application of fungicides,  
CC bactericides, nematocides, insecticides, or viricides) that are typically  
CC used by farmers for controlling the spread of plant pathogens and  
CC providing protection against disease causing pathogens. The method  
CC contributes to the production of high quality and high yield agricultural  
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
CC having reduced spots, blemishes and blotches that are caused by  
CC pathogens, agricultural products with increased shelf-life and reduced  
CC handling costs and high quality and yield crops for agricultural  
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis  
CC thaliana CDPK2 of the invention.  
XX  
XX Sequence 495 AA;  
SQ

Query Match  
Best Local Similarity 100.0%; Score 2593; DB 23; Length 495;  
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKENRRPSNTVLRYQTPRLRDHYLKKLGQGGQFGTYLCTEKSTSANVACKSIPIKR 60  
DB 1 METKENRRPSNTVLRYQTPRLRDHYLKKLGQGGQFGTYLCTEKSTSANVACKSIPIKR 60  
QY 61 KLVCREDYEDVWREIQIMHLLSEHPNVVRIKGTYESDVFVHVMVEVCGGELFDRIVSKG 120  
DB 61 KLVCREDYEDVWREIQIMHLLSEHPNVVRIKGTYESDVFVHVMVEVCGGELFDRIVSKG 120  
QY 121 HFSREAVKLITILGVVEACHSLGVHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKP 180  
DB 121 HFSREAVKLITILGVVEACHSLGVHRLDKPENFLFDSPKDDAKLKATDFGLSVFYKP 180  
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DB 181 GOYLYDVVGGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240  
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DB 241 GKLPDKSPDPTTISEAAKDLTYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVL 300  
QY 301 SRLKQFSQNNKIKKALRVIAERISEEIGGKELFKMIDTNSGTITFEELKAGLKRVG 360  
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DB 361 SELMESEIKSLMDAADINSGTIDYGEFLAATLHNNKVEREILVAAFSDFDKDGSYIT 420  
QY 421 IDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEPTAMVRKGDGVGRSRTMMKNLNF 480  
DB 421 IDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEPTAMVRKGDGVGRSRTMMKNLNF 480  
QY 481 NIADAFGVGDKSDD 495  
DB 481 NIADAFGVGDKSDD 495

RESULT 2  
AAG35776  
ID AAG35776 standard; Protein; 501 AA.  
XX  
XX AAG35776;  
AC  
XX 18-OCT-2000 (first entry)  
DT  
XX Arabidopsis thaliana protein fragment SEQ ID NO: 43753.  
DE  
XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX  
XX Arabidopsis thaliana.  
OS  
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PN  
XX EP1033405-A2.  
XX  
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PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 94.8%; Score 2458; DB 21; Length 501;
Best Local Similarity 94.8%; Pred. No. 2.4e-210;
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 4 KPNRRPSNTVLPYQTRLRDRHYLLGKLGQGGTGYTLCTEKTSANYACKSIPKRLV 63
Db 3 KPNRRPSNSVLPYETRLRDRHYLLGKLGQGGTGYTLCTEKSSANYACKSIPKRLV 62
Qy 64 CREDYEDVWREIQIMHLSHPNVVR1KGTVEDSVFVHI VMEVCEGGELFDRIVSKGHFS 123
Db 63 CREDYEDVWREIQIMHLSHPNVVR1KGTVEDSVFVHI VMEVCEGGELFDRIVSKGCFS 122
Qy 124 EREAVKLIKTILGVVEACHSLGVNMRDLKPNFLDPSKODAKLKATDFGLSVFYKQGY 183
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Db 123 EREAALIKITILGVVEACHSLGVNHRDLKPNFLFSDSPDAKLKATDFGLSVFYKPGQY 182  
Qy 184 LYDVVGSPIYVAPEVLKCCYGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243  
Db 183 LYDVVGSPIYVAPEVLKCCYGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242  
Qy 244 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPKPLDPAVLRL 303  
Db 243 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPKPLDPAVLRL 302  
Qy 304 KQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 363  
Db 303 KQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 362  
Qy 364 MESEIKSLMDAADIIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 423  
Db 363 MESEIKSLMDAADIIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 422  
Qy 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKRGDGVGRSRTMMKNLNFNIA 483  
Db 423 LOOACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKRGDGVGRSRTMMKNLNFNIA 482  
Qy 484 DAFGVDG----EKSD 495  
Db 483 EAFGVEDTSSTAKSD 498

## RESULT 3

AAM48001  
ID AAM48001 standard; Protein; 501 AA.

XX AC AAM48001;

DT 08-MAR-2002 (first entry)

XX DE Arabidopsis CDPK4 SEQ ID NO 3.

XX KW Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;  
XX KW disease resistance; agricultural; pathogen; crop yield; ornamental;  
XX KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;  
XX KW transgenic; plant; enzyme.

XX OS Arabidopsis thaliana.

XX PN WO200184911-A1.

XX PD 15-NOV-2001.

XX PF 04-MAY-2001; 2001WO-US14368.

XX PR 05-MAY-2000; 2000US-201925P.

XX PA (GEO ) GEN HOSPITAL CORP.

XX PI Sheen J;

XX DR WPI; 2002-062179/08.

XX DR N-PSDB; ABA06022.

XX PT Producing plant having increased disease resistance, comprises  
PT regenerating plant from a non-naturally occurring plant cell  
PT over-expressing a polynucleotide encoding a calcium dependent protein  
PT kinase polypeptide

XX PS Disclosure; Fig 2; 44pp; English.

XX CC The invention relates to producing a plant having increased disease  
CC resistance, comprising providing a non-naturally occurring plant cell  
CC over-expressing a polynucleotide encoding a calcium dependent protein  
CC kinase (CDPK) polypeptide and regenerating a plant from the plant  
CC cell, where the CDPK polypeptide is expressed in the plant, increasing  
CC the resistance of the plant to disease as compared to a  
CC naturally-occurring plant. The method is useful for a variety of

CC agricultural and commercial purposes including improving a plant's  
CC resistance against plant pathogens, increasing crop yields, improving  
CC crop and ornamental quality and reducing agricultural production costs.  
CC The method facilitates an effective and economical method for in-plant  
CC protection against plant pathogen, reducing or minimising the need for  
CC traditional chemical practices (e.g. application of fungicides,  
CC bactericides, nematocides, insecticides, or viricides) that are typically  
CC used by farmers for controlling the spread of plant pathogens and  
CC providing protection against disease causing pathogens. The method  
CC contributes to the production of high quality and high yield agricultural  
CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
CC having reduced spots, blemishes and blotches that are caused by  
CC pathogens, agricultural products with increased shelf-life and reduced  
CC handling costs and high quality and yield crops for agricultural  
CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
CC (e.g. fiber crops) purposes. The present sequence is that of Arabidopsis  
CC thaliana CDPK4 of the invention.

XX SQ Sequence 501 AA;

Query Match 94.8%; Score 2458; DB 23; Length 501;  
Best Local Similarity 94.8%; Pred. No. 2.4e-210;  
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

Qy 4 KPNRPRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPKRLV 63  
Db 3 KPNRPRPSNVLPYETPRLRDHYLLGKLGQGGFGTTYLCTEKSSANVACKSIPKRLV 62  
Qy 64 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKGHS 123  
Db 63 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFVHIVMEVCEGELFDRIVSKGCS 122  
Qy 124 EREAVKLITILGVVEACHSLGVNHRDLKPNFLFSDSPDAKLKATDFGLSVFYKPGQY 183  
Db 123 EREAALIKITILGVVEACHSLGVNHRDLKPNFLFSDSPDAKLKATDFGLSVFYKPGQY 182

Qy 184 LYDVVGSPIYVAPEVLKCCYGEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243  
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Qy 244 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPKPLDPAVLRL 303  
Db 243 DFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPKPLDPAVLRL 302

Qy 304 KQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 363

Db 303 KQFSQMNKIKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLRKVGSEL 362

Qy 364 MESEIKSLMDAADIIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 423

Db 363 MESEIKSLMDAADIIDNSGTTIDYGFLLAATLHMKNWEEELVAAFSDFDKDGSYITIDE 422

Qy 424 LOSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKRGDGVGRSRTMMKNLNFNIA 483

Db 423 LOOACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMKRGDGVGRSRTMMKNLNFNIA 482

Qy 484 DAFGVDG----EKSD 495

Db 483 EAFGVEDTSSTAKSD 498

## RESULT 4

AAG35777

ID AAG35777 standard; Protein; 425 AA.

XX AC AAG35777;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 43754.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.  
XX Arabidopsis thaliana.  
XX EP1033405-A2.  
XX PD 06-SEP-2000.  
XX XX 25-FEB-2000; 2000EP-0301439.  
XX 25-FEB-1999; 99US-0121825.  
XX 05-MAR-1999; 99US-0123180.  
XX 09-MAR-1999; 99US-0123548.  
XX 23-MAR-1999; 99US-0125788.  
XX 25-MAR-1999; 99US-0126264.  
XX 29-MAR-1999; 99US-0126785.  
XX 01-APR-1999; 99US-0127462.  
XX 06-APR-1999; 99US-0128234.  
XX 08-APR-1999; 99US-0128714.  
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XX 19-APR-1999; 99US-0130077.  
XX 21-APR-1999; 99US-0130449.  
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PR 01-JUL-1999; 99US-0141842.  
PR 01-JUL-1999; 99US-0142154.  
PR 02-JUL-1999; 99US-0142055.  
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PR 27-AUG-1999; 99US-0151065.  
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PR 07-SEP-1999; 99US-0152263.

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PR 10-SEP-1999; 99US-0153070.
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PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
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PR 29-SEP-1999; 99US-0156596.
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PR 21-OCT-1999; 99US-0160770.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
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PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 79.6%; Score 2064; DB 21; Length 425;
Best Local Similarity 94.5%; Pred. No. 2,7e-175;
Matches 399; Conservative 6; Mismatches 13; Indels 4; Gaps 1;

QY 78 MHHLSEHPNVVRIRKGTVEDSVFVHIVMEVCEGGELFDRIVSKGHFSREAVKLIKTLGV 137
DB 1 MHHLSEHPNVVRIRKGTVEDSVFVHIVMEVCEGGELFDRIVSKGCFSEAAKLIKTLGV 60

QY 138 VEACHSLGVNHRDLKPNFLFDPSPKDDAKLKATDFGLSVFYKPGQYLYDVVGGPYVAPE 197
DB 61 VEACHSLGVNHRDLKPNFLFDPSPDDAKLKATDFGLSVFYKPGQYLYDVVGGPYVAPE 120

QY 198 VLKCKYGPEDVNSAGVILILSGVPPFWAETESGIFRQILQCKLDFKSDPWTISEAA 257
DB 121 VLKCKYGPEDVNSAGVILILSGVPPFWAETESGIFRQILQCKLDFKSDPWTISEGA 180

QY 258 KDLIYKMLRSPKKRISAEALCHPWIVDEOAPDKPLDPAVLRLKQFSQMKIKOMAL 317
DB 181 KDLIYKMLRSPKKRISAEALCHPWIVDEHAPDKPLDPAVLRLKQFSQMKIKOMAL 240

QY 318 RVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLRKVGSELMESEIKSLMDAADI 377
DB 241 RVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLRKVGSELMESEIKSLMDAADI 300

QY 378 DMSGTIDYGEFLAATLHMKWREBEILVAAFSDFDKDGGYIITIDELQSACTEFGLCDTP 437
DB 301 DMSGTIDYGEFLAATLHMKWREBEILVAAFSDFDKDGGYIITIDELQSACTEFGLCDTP 360
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QY 438 LDDMIKEIDLNDGKIDFSEFTAMMRKGGVGRSRTMMKNLNFNIADAFGVDG---EKS 493
DB 361 LDDMIKEIDLNDGKIDFSEFTAMMRKGGVGRSRTMMKNLNFNIADAFGVDG---EKS 420
QY 494 DD 495
DB 421 DD 422

RESULT 5
AAW93256
ID AAW93256 standard; Protein; 512 AA.
XX
AC AAW93256;
XX
DT 25-AUG-1999 (first entry)
XX
DE Soybean CDPK protein.
XX
KW CDPK; calcium dependent protein kinase; tobacco; pathogen; invasion;
KW induction; elicitor; plant; disease resistance; parasiticide; soybean;
KW elicitor.
XX
OS Glycine max.
XX
FH Key Location/Qualifiers
FT Region 41..46
FT /note= "protein kinase sequence"
FT Region 158..163
FT /note= "protein kinase sequence"
FT Region 198..205
FT /note= "protein kinase sequence"
FT Binding-site 348..360
FT /note= "calcium binding site"
FT Binding-site 388..399
FT /note= "calcium binding site"
FT Binding-site 425..435
FT /note= "calcium binding site"
FT Binding-site 458..468
FT /note= "calcium binding site"
XX
PN W09902655-A1.
XX
PD 21-JAN-1999.
XX
PF 07-JUL-1998; 98WO-US14109.
XX
PR 08-JUL-1997; 97US-0889655.
XX
PA (KENT ) UNIV KENTUCKY RES FOUND.
XX
PI Chappell J, Lusso MFG;
XX
DR WPI; 1999-120859/10.
XX
PT New polynucleotides based on calcium dependent protein kinase genes
XX - useful to induce disease resistance in plants
XX
PS Example 4; Fig 4; 51pp; English.
XX
CC This invention describes a novel nucleic acid molecule and its encoded
CC protein that are induced upon pathogen invasion or elicitor treatment.
CC The products of the invention are functional in plants, plant tissue and
CC in plant cells for inducible gene expression and altering the disease
CC resistance phenotype of plants. The products of the invention are
CC related to calcium dependent protein kinase (CDPK) genes. The invention
CC describes the isolation of a novel tobacco CDPK protein fragment and its
CC encoding nucleic acid, isolated from a cell suspension culture derived
CC from a tobacco cultivar KY14 explant, after growth in the presence of
CC the elicitor parasiticide. This sequence represents the soybean CDPK
CC protein which is used in the description of the method.
XX
SQ Sequence 512 AA;
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[illegible]

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PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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QY 164 DAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKCKYGPEDVMSAGVILYLLSGV 223
Db 61 DAKLKATDFGLSVFYKPGQYLYDVVGSPYYVAPEVLKCKYGPEDVMSAGVILYLLSGV 120

QY 224 PPEWAETESGIFRQILQGLKDFKSDPWTISEAAKDLIYKMLERSPKKRISAHEALCPW 283
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QY 284 IVDEQAAPDKPLDPVLSRLKQFSQMNKIKKMLRVIAERLSPEEIGGLKELFKWIDTN 343
Db 181 IVDEHAAPDKPLDPVLSRLKQFSQMNKIKKMLRVIAERLSPEEIGGLKELFKWIDTN 240

QY 344 SGTITFEELKAGLRVGSSELMSESEIKSLMDAADIDNSGTIDYCEFLAATLHMNKWEREEI 403
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QY 404 LVAAFSDFDKDGGYITIDELQSACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAMMR 463
Db 301 LVVAFSYFDKGGYITIDELQSACTEFLGCDTLPDDMIKEIDLNDGKIDFSEFTAMMR 360

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RESULT 7
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AC AAG31158;
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XX 17-OCT-2000 (first entry)
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
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Query Match 67.2%; Score 1742; DB 21; Length 483;
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DB 4 NPDNOAYVVLGHKTNRIDYLSRKLGGQGGTGYLCTEIASGVDAACKSISKRKLISK 63

QY 66 EDYEDVREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGGELEFDRIIVSKGHFSR 125
DB 64 EDVEDVREIQIMHLAGHSIVTIKAGYEDSLYVHIVMELCAGGELEFDRIIVGHYSR 123

QY 126 EAVKLITILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQVLY 185
DB 124 KAAELTKIIVGVVEACHSLGVNHRDLKPNFLVKNDDDFSLKATDFGLSVFYKPGQVLY 183

QY 186 DVVGSPPYVAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFROILOGKLD 245
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QY 246 KSDPMTPTISEAAKLIYKMLERSPKKRISAEHALCHPMIVDSQAPDKPLDPAVLRLKQ 305
DB 244 ESDPMPVLSDSAKLIRMLSKPRLTAHEVLRHPWICENGVAAPDRALDPAVLRLKQ 303

QY 306 FSQMKIKKMLRVIAERLSEEEIGGLKELFMIDTNSGTITFEELKAGLRKRVGSELME 365
DB 304 FSAMNKLKMLKVAIESLSEEEIAGLREMFQAMDTNSGATITFDELKAGLRKRVGSELME 363

QY 366 SEIKSLDAADIDNSGTTIDYGEFLAATLHMKNWEEELVAAFSDFDKGSGYITIDELQ 425
DB 364 TEIHDLMDRADVDNSGTTIDYGEFLAATLHMLKLEELVAAFOYFDKDGSGYITIDELQ 423

QY 426 SACTEFGCLDTPDDMIKEIOLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNAD 484
DB 426 SACTEFGCLDTPDDMIKEIOLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNAD 484
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QY 485 A 485
Db 483 A 483

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ID AAG31157 standard; Protein; 556 AA.
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AC AAG31157;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 37371.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Qy 246 KSDPMTTISEAAKDLIYKMLERSPKKRISAHEALCHPMIVDEQAAPKPLDPAVLRLKQ 305  
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XX 18-OCT-2000 (first entry)  
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XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.  
XX Arabidopsis thaliana.  
OS Arabidopsis thaliana.  
XX EP1033405-A2.  
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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
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Query Match 65.7%; Score 1703; DB 21; Length 1017;

Best Local Similarity 65.7%; Pred. No. 1.5e-142;

Matches 323; Conservative 64; Mismatches 81; Indels 24; Gaps 2;

Qy 2 ETXPNRRP-----SNTVLPYQTPRLRDHYLKGKLGQGFQGTYYLCTEKSTS 49.

Db 509 ETKAEPQKPKHMRVSSAGLRTESVLQRKTENKFYSLGRKLGQGFQGTYYLCTEKSTS 568





environmental stress; salinity; drought; temperature; tolerance;  
transgenic plant; EST; expressed sequence tag.

Physcomitrella patens.

WO200177356-A2.

18-OCT-2001.

06-APR-2001; 2001WO-US11435.

07-APR-2000; 2000US-196001P.

(BAD1) BASF PLANT SCI GMBH.

Da Costa Silva EO, Bohnert HJ, Van Thiel N, Chen R;

Sarria-Millan R;

WPI; 2002-049153/06.

N-PSDB; ABA91081.

New protein, useful for increasing tolerance to environmental stress,  
comprises a Protein Kinase Stress-Related Protein selected from  
Protein Kinases, Casein Kinase homologs, MAP Kinases or Calcium  
dependent protein kinases -

Claim 13; Fig 3W; 154pp; English.

Sequences AAM52830-AAM52842 represent novel protein kinase stress-related  
proteins (PKSRPs) from the moss *Physcomitrella patens*, and sequences  
ABA91069-ABA91081 represent full-length cDNAs encoding them. The cDNA  
sequences were obtained from expressed sequence tags (ESTs; ABA91056-  
ABA91068) derived from *Physcomitrella patens* cDNA libraries. The PKSRPs  
of the invention comprise protein kinase-6 (PK-6), protein kinase-7  
(PK-7), protein kinase-8 (PK-8), protein kinase-9 (PK-9), casein kinase  
homologue-1 (CK-1), casein kinase homologue-2 (CK-2), casein kinase  
homologue-3 (CK-3), mitogen-activated protein (MAP) kinase-2 (MPK-2),  
MAP kinase-3 (MPK-3), MAP kinase-4 (MPK-4), MAP kinase-5 (MPK-5),  
calcium-dependent protein kinase-1 (CPK-1), and calcium-dependent protein  
kinase-2 (CPK-2). When overexpressed, the PKSRPs are able to confer  
tolerance to environmental stresses such as salinity, drought,  
temperature, metal, chemical, pathogenic and oxidative stress.  
*Physcomitrella patens* PKSRP nucleic acids may be used to generate  
transgenic plants and seeds with increased tolerance to salinity, drought  
and temperature. The transgenic plants generated can be monocots or  
dicots and are especially maize, wheat, rye, oat, triticale, rice,  
barley, cotton, rapeseed, cassava, sunflower, tagetes, leguminous plants  
(e.g., soybean, peanut, *Vicia species*, alfalfa), solanaceous plants  
(e.g., potato, tobacco, aubergine, pepper, tomato), coffee, cacao, tea,  
*Salix species*, oil palm, coconut, perennial grasses and forage crops. The  
PKSRP nucleotide and proteins may also be used in evolutionary and  
protein structural studies and as markers for specific regions of  
the genome.

Sequence 549 AA;

Query Match 58.2%; Score 1509.5; DB 23; Length 549;

Best Local Similarity 60.8%; Pred. No. 1.1e-125;

Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

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Db 69 PRPKASRSVSGVLGKPLSDIOSYILGRELGRGQGVTVLCTDRMTNEAYACKSIARKK 128  
QY 62 LVCREDEYVREIQIMHLLSEHPNVVRIGKTVEDSVFVHVMVECGEGGFDFRIVSKGH 121  
Db 129 LTKSKEDIEDKREVMQHMLSGTPNVLVKDVEDKSHVHVLNLCAGGELFRIITAKGH 188  
QY 122 FSREAVLKTKTLGVVEACHSLGVVHMRDLKPNFLFDPSPKDAKLIKATDFGLSVFKPG 181  
Db 189 YSERAAADMCRIWVNVHRSGLGVFHRDLKPNFLLASKAEDAPLKATDFGLSTFFKPG 248  
QY 182 QVLYDVVGSPYYVAPEVLKCKYCPEDVMSAGVILYILLGVPPFFWAEATESGIFRILQG 241

Db 249 DVFQDIVGSAYYVAPEVLKRSYGPADVNSAGVIVYILLGVPPFWAEETEGCIDEAVLKG 308  
QY 242 KLDPKSDPWTITSEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLS 301  
Db 309 HIDFENDPWPKISNGAKDLVRKLNPNVKIRLTAQQLVNLHPMKEDGADPDVPLDNAVL 368  
QY 302 RLKQFSQMNKIKKWLARVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRKVS 361  
Db 369 RLKNFSAANKMKLALKLVIAESUSEEIVGLREMFKSIDTNSGTITFEELKEGLKOGS 428  
QY 362 ELMESEIKSLMDAADIDNSGTIDYGEFLAATLHNNKMEREEILVAAFSDFDKDCSGYITI 421  
Db 429 KLNESDIRKLMEAADVDGNGKIDNFENFISATMMNKTEKEDHLWAAEFHFDTNSGYITI 488  
QY 422 DELQSACTEFLGCD-TPLDDMIKEIDLNDGKIDFSEFTAMRRKGD-GVGRSRTMMK 476  
Db 489 DELQEAEMKNGMGDPETIQBIISVDTNDNGRIDYDEFVAMRRKNGPNAENGVTNK 545

RESULT 14

AAG31159

ID AAG31159 standard; Protein; 408 AA.

XX AC AAG31159;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 37373.

XX KW Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX KW termination sequence.

XX OS Arabidopsis thaliana.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

XX PR 23-MAR-1999; 99US-0125788.

XX PR 25-MAR-1999; 99US-0126264.

XX PR 29-MAR-1999; 99US-0126785.

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PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.





GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 43 Seconds  
(without alignments)  
1107.058 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593  
Sequence: 1 METKNPRPSNTVLPYQTP.....KNLNFNIADAFVGDEKSD 495

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 76:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
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2	2458	94.8	501	G85097	hypothetical prote
3	2030	78.3	490	T08873	calcium-dependent
4	1944	75.0	508	A43713	calcium-dependent
5	1847.5	71.2	490	S71776	calcium-dependent
6	1752	67.6	492	T03271	calcium-dependent
7	1751	67.5	487	S71770	calcium-dependent
8	1745	67.3	554	T03263	calcium-dependent
9	1742	67.2	556	T06126	calcium-dependent
10	1731	66.8	544	D84550	calcium-dependent
11	1724	66.5	610	A49082	probable calmoduli
12	1709.5	65.9	573	T03940	calcium-dependent
13	1700.5	65.6	484	T05650	calcium-dependent
14	1672.5	64.5	639	T02784	calcium-dependent
15	1640.5	63.3	583	H84810	calcium-dependent
16	1630	62.9	451	S56717	probable calcium-d
17	1586	61.2	542	S56651	calcium-dependent
18	1484.5	57.3	540	T01989	calcium-dependent
19	1482	57.2	531	D85059	calcium-dependent
20	1482	57.2	533	S56652	probable calcium d
21	1480	57.1	531	T02993	calcium-dependent
22	1463.5	56.4	521	G94543	calcium-dependent
23	1462	56.4	529	S71774	calcium-dependent
24	1460.5	56.3	513	T02259	calcium-dependent
25	1460	56.3	534	JC1515	calcium-dependent
26	1458.5	56.2	538	T08874	calcium-dependent
27	1449	55.9	554	T05476	calcium-dependent
28	1437.5	55.4	465	T03024	calcium-dependent
29	1432.5	55.2	532	T14335	protein kinase, ca

ALIGNMENTS

RESULT 1

S46284

calcium-dependent protein kinase (EC 2.7.1.-) 2 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 16-Jun-2000

C:Accession: S46284

R:Urao, T.; Katagiri, T.; Mizoguchi, T.; Yamaguchi-Shinozaki, K.; Hayashida, N.; Shino;

Mol. Gen. Genet. 244, 331-340, 1994

A:Title: Two genes that encode Ca(2+)-dependent protein kinases are induced by drought

A:Reference number: S46283; MUID:94359455; PMID:8078458

A:Accession: S46284

A:Molecule type: mRNA

A:Residues: 1-495 <URA>

A:Cross-references: EMBL:D21806; NID:gi235717; PIDN:BAA04830.1; PID:g604881

C:Gene: CDPK2

C:Superfamily: calcium-dependent protein kinase

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif;

F:24-284/Domain: protein kinase ATP-binding motif

F:327-359/Domain: calmodulin repeat homology <EF1>

F:363-395/Domain: calmodulin repeat homology <EF2>

F:399-431/Domain: calmodulin repeat homology <EF3>

F:433-465/Domain: calmodulin repeat homology <EF4>

F:55/Active site: Lys #status predicted

Query Match 100.0%; Score 2593; DB 1; Length 495;  
Best Local Similarity 100.0%; Pred. No. 1.7e-89;  
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKNPRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPIKR 60

DB 1 METKNPRPSNTVLPYQTPRLRDHYLLGKLGQGGFGTTYLCTEKSTSANVACKSIPIKR 60

QY 61 KLVCRDEYEDVWREIQIMHLSHNVPVRIKCTYEDSVFVHVMVECEGELFDRIVSKG 120

DB 61 KLVCRDEYEDVWREIQIMHLSHNVPVRIKCTYEDSVFVHVMVECEGELFDRIVSKG 120

QY 121 HFSREAVKLIKTLGVWEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKFP 180

DB 121 HFSREAVKLIKTLGVWEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKFP 180

QY 181 GGYLDVGVSPYYVAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQ 240

DB 181 GGYLDVGVSPYYVAPEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQ 240

QY 241 GKLDFKSPWPMTISEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPKPLDPAVL 300

DB 241 GKLDFKSPWPMTISEAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPKPLDPAVL 300

QY 301 SRLKQFSQMKIKQALRVIAERLSEETGGIKELFKMIDTNSGTITFEELKAGLKRVG 360

|||||

Db 301 SRLKQFSQMNKIKKXALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVG 360  
Qy 361 SELMESEIKSLMDAADINSCTIDYGEFLAATLHNMKMEREEILVAAPSFDFDKDGGSYIT 420  
Db 361 SELMESEIKSLMDAADINSCTIDYGEFLAATLHNMKMEREEILVAAPSFDFDKDGGSYIT 420  
Qy 421 IDELOQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480  
Db 421 IDELOQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480  
Qy 481 NIADAFGVGDGKSD 495  
Db 481 NIADAFGVGDGKSD 495

RESULT 2  
G85097  
hypothetical protein AT4g09570 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 23-Mar-2001  
C:Accession: G85097  
R:anonymouse, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: G85097  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-501 <STO>  
A:Cross-references: GB:NC\_001268; NID:G7267652; PIDN:CAB78080.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: At4g09570  
A:Map position: 4  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C:Keywords: EF hand

Query Match 94.8%; Score 2458; DB 2; Length 501;  
Best Local Similarity 94.8%; Pred. No. 1.7e-84;  
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;  
Qy 4 KPNPRPSNVLVPYQTPRLRDHYLLGKLGQGGTGTYLCTEKSTSNANYACKSIPKRLKLV 63  
Db 3 KPNPRPSNVLVPYQTPRLRDHYLLGKLGQGGTGTYLCTEKSSSNANYACKSIPKRLKLV 62  
Qy 64 CRDIEDVREIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGELEFDRIVSKGHFS 123  
Db 63 CRDIEDVREIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGELEFDRIVSKGCF 122  
Qy 124 EREAVKLITLGVVEACHSLGVWHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKPGQY 183  
Db 123 EREAVKLITLGVVEACHSLGVWHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKPGQY 182  
Qy 184 LYDVVGSPPYVAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 243  
Db 183 LYDVVGSPPYVAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLK 242  
Qy 244 DFKSDPWTPTISEAAKOLIIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLPAVLRL 303  
Db 243 DFKSDPWTPTISEAAKOLIIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLPAVLRL 302  
Qy 304 KQFSQMNKIKKXALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSEL 363  
Db 303 KQFSQMNKIKKXALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSEL 362  
Qy 364 MESEIKSLMDAADINSCTIDYGEFLAATLHNMKMEREEILVAAPSFDFDKDGGSYITIDE 423  
Db 363 MESEIKSLMDAADINSCTIDYGEFLAATLHNMKMEREEILVAAPSFDFDKDGGSYITIDE 422  
Qy 424 LQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFNTA 483  
Db 423 LQACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNFNTA 482  
Qy 484 DAFGVGDG----BKSD 495

Db 483 EAFGVEDTSSTAKSD 498  
RESULT 3  
T08873  
calcium-dependent protein kinase (EC 2.7.1.1-) beta - soybean  
C:Species: Glycine max (soybean)  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jan-2000  
C:Accession: T08873  
R:Lee, J.Y.; Yoo, B.C.; Harmon, A.C.  
submitted to the EMBL Data Library, September 1996  
A:Reference number: Z16505  
A:Accession: T08873  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-490 <LEE>  
A:Cross-references: EMBL:U69173; NID:G2501763; PID:G2501764  
C:Genetics:  
A:Gene: CDPK beta  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specif  
F:22-282/Domain: protein kinase homology <KIN>  
F:30-38/Region: protein kinase ATP-binding motif  
F:324-356/Domain: calmodulin repeat homology <EFH>  
F:53/Active site: Lys #status predicted  
Query Match 78.3%; Score 2030; DB 2; Length 490;  
Best Local Similarity 81.1%; Pred. No. 1.1e-68;  
Matches 386; Conservative 43; Mismatches 45; Indels 2; Gaps 2;  
Qy 14 VLPVQTPRLRDHYLLGKLGQGGTGTYLCTEKSTSNANYACKSIPKRLKLVCREDYEDVWR 73  
Db 12 VLPVQTPARLADHYLLGKLGQGGTGTYLCTHKVTGKLYACKSIPKRLKLVQCEYDDVWR 71  
Qy 74 EIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGELEFDRIVSKGHFSEREAVKLK 133  
Db 72 EIQIMHLSHPNVRIKGTYESVVFHIVMEVCEGGELEFDRIVSKGHFSEREAVKLK 131  
Qy 134 ILGVVEACHSLGVWHRDLKPEFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
Db 132 ILGVVEACHSLGVWHRDLKPEFLFDSPTGSDAQMKATDFGLSVILQARQAFHDVVGSPY 191  
Qy 194 VAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTPT 253  
Db 192 VAPEVLKCKYGPIDVMSAGVILYLLSGVPPFWAETESGIFRQILNGDDJDFVSEPPSI 251  
Qy 254 SEAAKOLIIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLPAVLRLKQFSQMNKIK 313  
Db 252 SENAKELVKQLDRDPKKRISAHEVLCNPWVDD-IAPDKPLDSAVLTRLKHFSAMNKLK 310  
Qy 314 KXALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMESEIKSLMD 373  
Db 311 KXALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKEGLKSVGNSLMESEIKSLME 370  
Qy 374 AADINDSGTIDYGEFLAATLHNMKMEREEILVAAPSFDFDKDGGSYITIDELOQACTEFLG 433  
Db 371 AADINDSGTIDYGEFLAATLHNMKMEREEILVAAPSFDFDKDGGSYITIDELOQACDFSL 430  
Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNTADAFV 488  
Db 431 GDVHLDDEMIKEIQDNDGRIDVAEFAAMMKKGGPNMGRSRTMKGNLNFNTADAFGM 486

RESULT 4  
A43713  
calcium-dependent protein kinase (EC 2.7.1.1-) - soybean  
C:Species: Glycine max (soybean)  
C:Date: 03-Mar-1993 #sequence\_revision 14-Jul-1994 #text\_change 11-Jun-1999  
C:Accession: A43713  
R:Harper J.F.; Suesman, M.R.; Schaller, G.E.; Putnam-Evans, C.; Charbonneau, H.; Harm  
Science 252, 951-954, 1991  
A:Title: A calcium-dependent protein kinase with a regulatory domain similar to calmod

submitted to the EMBL Data Library, February 1995

A:Description: Expression of the calcium-dependent protein kinase gene family in Arabid

A:Reference number: S71197

A:Accession: S71902

A:Molecule type: DNA

A:Residues: 1-164,'S',166-239,'E',241-300,'KF',303-350,'S',352-490 <HOW>

A:Cross-references: EMBL:U20626; NID:g836945; PIDN:AAA67657.1; PID:g836946

R:Hong, Y.; Takano, M.; Liu, C.M.; Gasch, A.; Chye, M.L.; Tan, C.T.; Koh, C.C.; Chua, N

submitted to the EMBL Data Library, January 1995

A:Description: Expression of the calcium dependent protein kinase gene family in Arabid

A:Reference number: S71196

A:Accession: S71196

A:Molecule type: mRNA

A:Residues: 1-164,'S',166-239,'E',241-300,'KF',303-350,'S',352-490 <HOA>

A:Cross-references: EMBL:U20398; NID:g836937; PIDN:AAA67653.1; PID:g836938

C:Genetic: CDPK9

A:Introns: 177/1; 225/1; 276/1; 370/3; 445/3

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k

C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specifi

F:20-280/Domain: protein kinase homology <KN>

F:28-36/Region: protein kinase ATP-binding motif

F:323-355/Domain: calmodulin repeat homology <EF1>

F:359-391/Domain: calmodulin repeat homology <EF2>

F:395-427/Domain: calmodulin repeat homology <EF3>

F:429-461/Domain: calmodulin repeat homology <EF4>

F:51/Active site: Lys #status predicted

Query Match	71.2%	Score 1847.5;	DB 1;	Length 490;
Best Local Similarity	73.5%;	Pred. No. 5.8e-62;		
Matches 355;	Conservative 52;	Mismatches 69;	Indels 7;	Gaps 2;
QY 1	METKNPRPSNTVLPTQYPRLRDHYLLKGLQGQGGTTVLTCTEKTSTANYACKSI	PKR 60		
Db 1	MANKPRTR----WVLPTKTKNVDNVLFGVLGGQGGTFLCTHKQTGQKLACKSI	PKR 56		
QY 61	KLVCREDYEDVWREIQIMHLSHPNVNRIKGTVEDSVFVHIVMEVCGGELFDRIVSKG	120		
Db 57	KLLCQEDYDVLREIQIMHLSYPPNVRIESAYEDTKNVHLVMELCGGELFDRIVKRG	116		
QY 121	HFSERAEVKLIITILGVBAACHSLGVNHRDLKPNFLDFSPKDDAKLKATDFGLSVFYKP	180		
Db 117	HYSEREAALKIITIVGVBAACHSLGVVHRLKPNFLFSSDDEASLKATDFGLSVFCTP	176		
QY 181	GOYLDVVGSPYVVAPEVLKCCGPEIDVMSAGVILYILSGVPFVAETESGIFRQILQ	240		
Db 177	GAFLSGVSAIYVVAPEVLHKKHVGPCDVMASGVILYILCGPPFPFAESIGIFRKLILQ	236		
QY 241	GKLDPKSDPWPITSEAAKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVL	300		
Db 237	GKLDPEINPWPISISAKDLIKWLESNPKRLTAHQVLCHPWIVDDKVAADPKPLDCAVV	296		
QY 301	SRLKQFSQNNKIKKQALRVIAERLSSEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG	360		
Db 297	SRLKNGSAMNKLKQALRVIAERLSSEEIGGLKELFKMIDTDXSGTTITFEELKQGMRRVG	356		
QY 361	SELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNQVREERILVAAPDFDKDQSGVIT	420		
Db 357	SELMESEIQELLRAAADVDSGTTIDYGEFLAATLHNLKLEERENLVAAFPDFDKDASGVIT	416		
QY 421	IDELQSACTEFLGCDTPLDDMTKEIDLDNDGKIDFSEFTAMRKGDGVGRS--RTMMKN	477		
Db 417	IEELQAAKEFGINDSLNLDMDIKDIDQDNDGQIDYGEFVAMMRKNGTGGIGRRTMRS	476		
QY 478	LNF 480			
Db 477	LNF 479			

RESULT 6

T03271

calcium-dependent protein kinase (EC 2.7.1.-) 1 - maize

C:Species: Zea mays (maize)

C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 16-Jun-2000  
C:Accession: T03271  
R:Berberich, T.; Kusano, T.  
Mol. Gen. Genet. 254, 275-283, 1996  
A>Title: Cycloheximide induces a subset of low temperature-inducible genes in maize.  
A:Reference number: Z14873  
A:Accession: T03271  
A>Status: translated from GB/EMBL/DDBBJ  
A:Molecule type: mRNA  
A:Residues: 1-492 <BER>  
A:Cross-references: EMBL:D84408; PIDN:BAA12338.1  
A:Experimental source: strain honey bantum  
A>Note: low temperature-inducible  
C:Genetics:  
A:Gene: CDPKI

C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F:25-285/Domain: protein kinase homology <KN>  
F:33-41/Region: protein kinase ATP-binding motif  
F:328-360/Domain: calmodulin repeat homology <EF1>  
F:364-396/Domain: calmodulin repeat homology <EF2>  
F:400-432/Domain: calmodulin repeat homology <EF3>  
F:434-466/Domain: calmodulin repeat homology <EF4>  
F:56/Active site: Lys #status predicted

Query Match                  67.6%; Score 1752; DB 1; Length 492;  
Best Local Similarity      70.6%; Pred. No. 2e-58;  
Matches 334; Conservative    54; Mismatches 83; Indels    2; Gaps    2;

Qy 13 TVLPVQTPLRLDHYLGKGLGQQQGFGTYLTCTEKSTSNANYACKSIPIKRKLVCREDYDVW 72  
     :  
Db 14 SVLGHHTPNLRDLVALGRKLGGQGFQGTYYLTCTELATGIDYACKSISKRKLTKEDVDVVR 73  
     :  
Qy 73 REIQIMHHLSEHNVVRIKGTVSDSVFHVIMEVCEGELPDRIVSKGHFSEREAVKLK 132  
     :  
Db 74 REIQIMHLSGHKNVAIKAYEQDVTHIWMELCAGLEFDRIIQRGHSERKAALTR 133  
     :  
Qy 133 TLGVVEACHSLGVHMHRDLKPENFLDSPKDDAKLKATDFGLSFYFKPGQVLYDVVGSPY 192  
     :  
Db 134 IIVGVVEACHSLGVHMHRDLKPENFLANRDDLSLKALDFGLSVFFKPGQVFTDVVGSPY 193  
     :  
Qy 193 YVAPVLKKCYGEIDWSAGVILYLLSGVPFWAETESGI FROILQGLDKFSDPWPT 252  
     :  
Db 194 YVAPVELLKSYPADAWTAGVTLYTLTSGVPPFWAETQQGIFDAVLKGAIDFSDPWPV 253  
     :  
Qy 253 ISEAAKDLYTKMLERSPKRKISAHEALCHPMI VDEQAAPDKPLDPAVLSRLKQFSOMNKI 312  
     :  
Db 254 ISDSAKDLIRLMNPRAEHLTAHEVLCHPMIRDHGVAPORPDPAPVLSRIKQFSAMNKL 313  
     :  
Qy 313 KKMALRVIAERLSEEEIGGKELFKMDITDNSGTITFEELKAGLKRVSGLSEMESEIKSLM 372  
     :  
Db 314 KKMALRVIAESLEESEEIAGLKEMFQMTDMTNSGAI TYDELKEGLRKYGSTLKTDFEIRDLM 373  
     :  
Qy 373 DAADDINSGTI DYGEPLAATLHMNMWEREILVAASFDFDKGSGYITIDBLOACTEFFG 432  
     :  
Db 374 DAADDINSGTI DYIEFIATLHLUNKEREHLVAAFSYFDKGSGYITVDQLACKEHN 433  
     :  
Qy 433 LCDTPDLMIKEIDLNDNGKIDFSEFTAMMRKGD -GVGRSRRTMMNLNFNIAD 484  
     :  
Db 434 MPDAFLDDVINAEADQNDRIDYGEFVAMTMKGMVGR -RTWRNSLNISNRD 485  
     :

RESULT 7  
S71770  
calcium-dependent protein kinase (EC 2.7.1.-) - mung bean  
C:Species: Vigna radiata (mung bean)  
C>Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-Jun-1999  
C:Accession: S71770  
R:Botella, J.R.; Arteca, J.M.; Somodevilla, M.; Arteca, R.N.  
Plant Mol. Biol. 30, 1129-1137, 1996  
A>Title: Calcium-dependent protein kinase gene expression in response to physical and ch  
A:Reference number: S71770; UID:96311003; PMID:8704124  
A:Accession: S71770



F:464-96/Domain: calmodulin repeat homology <EF3>  
F:498-530/Domain: calmodulin repeat homology <EF4>  
F:120/Active site: Lys #status Predicted

Query Match		67.3%;	Score 1745;	DB 1;	Length 554;
Best Local Similarity		70.0%;	Pred. No. 3.9e-58;		
Matches 333;		Conservative 57;	Mismatches 84;	Indels 2;	Gaps 2;
QY	13	TVLPTPTLRDHYLLGKLGQGGQFGTTLCYCTEKSANYACKSIPKRLKLVCREYEDVM	72		
Db	78	SVLGHTPNRLDYLALGKLGQGGQFGTTLCYCTEKSANYACKSIPKRLKLVCREYEDVM	137		
QY	73	REIQMHHLSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVLIK	132		
Db	138	REIQMHHLSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVLIK	197		
QY	133	TILGVVEACHSLGVHMRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLYDVVGSY	192		
Db	198	IIVGVVEACHSLGVHMRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLYDVVGSY	257		
QY	193	YVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDFKSPWPT	252		
Db	258	YVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDFKSPWPT	317		
QY	253	ISEAAKOLIKYKMLERSPKKRIISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKI	312		
Db	318	ISDSAKOLIKYKMLERSPKKRIISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFSOMNKI	377		
QY	313	KQWALRVIAERLSEIEIGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSEIKSLM	372		
Db	378	KQWALRVIAERLSEIEIGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSEIKSLM	437		
QY	373	DAADINDNGTIDYGFELATLHMNMWEREELVAAFSDFDKGSGYITIDELQSACTEFG	432		
Db	438	DAADINDNGTIDYGFELATLHMNMWEREELVAAFSDFDKGSGYITIDELQSACTEFG	497		
QY	433	LCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIADAFG	487		
Db	498	MPDAFLDDVINEADQNDGRIDYGFVAMMTKGNMGVGR-RTMRNSLNISMIRDAPG	552		
RESULT 9					
T06126					
calcium-dependent protein kinase (EC 2.7.1.1.-) CPK5 - Arabidopsis thaliana					
N:Alternate names: protein F23E12.130					
C:Species: Arabidopsis thaliana (mouse-ear cress)					
C:Date: 30-Apr-1999 #sequence revision 30-Apr-1999 #text_change 21-Jan-2000					
C:Accession: T06126					
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, B.; Brandt, A.; Duesterhoeft, A.; Hoheisel, J.					
submitted to the Protein Sequence Database, April 1999					
A:Reference number: Z15485					
A:Accession: T06126					
A:Molecule type: DNA					
A:Residues: 1-556 <BEV>					
A:Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.130					
A:Experimental source: cultivar Columbia; BAC clone F23E12					
C:Genetics:					
A:Gene: CPK5; ATSP:F23E12.130					
A:Map position: 4					
A:Introns: 252/1; 300/1; 389/3; 445/3; 520/3					
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase					
F:95-355/Domain: protein kinase homology <KIN>					
F:398-430/Domain: calmodulin repeat homology <EF1>					
F:434-466/Domain: calmodulin repeat homology <EF2>					
F:470-502/Domain: calmodulin repeat homology <EF3>					
F:504-536/Domain: calmodulin repeat homology <EF4>					
Query Match		67.2%;	Score 1742;	DB 2;	Length 556;
Best Local Similarity		68.4%;	Pred. No. 5.1e-58;		
Matches 329;		Conservative 66;	Mismatches 84;	Indels 2;	Gaps 2;
QY	6	NPRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCYCTEKSANYACKSIPKRLKLVCR	65		

Db	77	NPDNQAYVVLGHKTPNIRDIYTLTKRKGQGGQFGTTLCYCTEKSANYACKSIPKRLKLVCR	136		
QY	66	EDYEDVWREIQMHHLSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVLIK	125		
Db	137	EDYEDVWREIQMHHLSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVLIK	196		
QY	126	EAVKLIKTLGVVEACHSLGVHMRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLY	185		
Db	197	KAELTKIIVGVVEACHSLGVHMRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLY	256		
QY	186	DVVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDF	245		
Db	257	DVVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILOKGLDF	316		
QY	246	KSDPPTTSEAAKOLIKYKMLERSPKKRIISAEALCHPWIVDEQAAPDKPLDPAVLRLKQ	305		
Db	317	ESDPMPVSDSADKILIRMLSSKPAERLTAHEVLRHPWICENGVAAPDRALDPAVLRLKQ	376		
QY	306	FQMNKIKQWALRVIAERLSEIEIGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSE	365		
Db	377	FSAMNKLKQWALRVIAERLSEIEIGLKELFKMIDTNSGTTTFEELKAGLRKRVGSELSE	436		
QY	366	SEIKSLMDAADINDSGTIDYGFELATLHMNMWEREELVAAFSDFDKGSGYITIDELQ	425		
Db	437	TEIHDMDAADVDNSGTTIDYSEFIAATLHNLKEREHLVAAFOYFDKDGSGFIIDELQ	496		
QY	426	SACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMKNLNFNIAD	484		
Db	497	QACVEHGMADVFLEIDIKEVDQNDGKIDYGFVEMQKGNAGVGR-RTMRNSLNISMIRD	555		
QY	485	A 485			
Db	556	A 556			
RESULT 10					
D84550					
probable calmodulin-domain protein kinase CPK6 [imported] - Arabidopsis thaliana					
C:Species: Arabidopsis thaliana (mouse-ear cress)					
C:Date: 02-Feb-2001 #sequence revision 02-Feb-2001 #text_change 02-Mar-2001					
C:Accession: D84550					
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;					
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, I.					
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,					
Nature 402, 761-768, 1999					
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.					
A:Reference number: A84420; MUID:20083487; PMID:10617197					
A:Accession: D84550					
A:Status: preliminary					
A:Molecule type: DNA					
A:Residues: 1-544 <STO>					
A:Cross-references: GB:A5002093; NID:2623752; PIDN:AAB86506.1; GSPDB:GN00139					
C:Genetics:					
A:Gene: At2g17290					
A:Map position: 2					
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein ki					
C:Keywords: EF hand					
Query Match		66.8%;	Score 1731;	DB 2;	Length 544;
Best Local Similarity		68.3%;	Pred. No. 1.3e-57;		
Matches 328;		Conservative 65;	Mismatches 85;	Indels 2;	Gaps 2;
QY	6	NPRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCYCTEKSANYACKSIPKRLKLVCR	65		
Db	65	NVDNQSYVVLGHKTPNIRDIYTLTKRKGQGGQFGTTLCYCTEKSANYACKSIPKRLKLVCR	124		
QY	66	EDYEDVWREIQMHHLSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVLIK	125		
Db	125	EDYEDVWREIQMHHLSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVLIK	184		
QY	126	EAVKLIKTLGVVEACHSLGVHMRDLKPNFLFDSPKDDAKLKATDFGLSVFVKPGQYLY	185		

Db 185 KAAELTKIIVGVVEACHSLGVMHRLDKPENFLLVNKDDDFSLKAIDFGLSVFFKPGQIFK 244  
QY 186 DVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFWAETSGSIFRQILQGLKDF 245  
Db 245 DVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFWAETSGSIFRQILQGLKDF 304  
QY 246 KSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCHPMIYDQOAPDKPLDPAVLSRLKQ 305  
Db 305 DTPWPVPSDSAKDLIRKMLCSPSERLTAHEVLRHWPICENGVAPODRAIDPAVLSRLKQ 364  
QY 306 FSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSGLME 365  
Db 365 FSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSGLME 424  
QY 366 SEIKSLMDAADIDNSGTIDYGEFLAATLHNKMKERIEILVAATSDPKDGSYTTIDELQ 425  
Db 425 TEIRDLMWAADVNSGTTIDYSEFIAATLHNKMKERIEILVAATSDPKDGSYTTIDELQ 484  
QY 426 SACTEFLGCDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTVMKMLNFNIAD 484  
Db 485 QSCIEHGMDVFLIEDIIEKVDQDNDGRIDYEEFVAMMOKGNAGVGR-RTMKNSLNTSMRD 543  
  
RESULT 11  
A49082  
calcium-dependent protein kinase (EC 2.7.1.1) AK1 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 11-Jun-1999  
C:Accession: A49082  
R:Harper, J.F.; Binder, B.M.; Sussman, M.R.  
Biochemistry 32, 3282-3290, 1993  
A:Title: Calcium and lipid regulation of an Arabidopsis protein kinase expressed in Esch  
A:Reference number: A49082; MUID:93213795; PMID:7916621  
A:Contents: ecotype Columbia  
A:Accession: A49082  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-610 <HAR>  
A:Cross-references: GB:14771; NID:G289189; PIDN:AAA32761.1; PID:G304105  
A>Note: sequence extracted from NCBI backbone (NCBI:128903, NCBI:128904)  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F:148-408/Domain: protein kinase homology <KIN>  
F:156-164/Region: protein kinase ATP-binding motif  
F:451-483/Domain: calmodulin repeat homology <EF1>  
F:487-519/Domain: calmodulin repeat homology <EF2>  
F:523-555/Domain: calmodulin repeat homology <EF3>  
F:557-589/Domain: calmodulin repeat homology <EF4>  
F:179/Active site: Lys #status Predicted  
  
Query Match 66.5%; Score 1724; DB 1; Length 610;  
Best Local Similarity 65.5%; Pred. No. 2.5e-57;  
Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;  
  
QY 2 ETKP-----NPRP-----SNTVLPYQTPRLDRHYLLGKLGQGGQGGTGY 41  
Db 106 ETKPSKPPDPAPKPKPKMKRVSSAGLATESVLQKRTNFKEFVSLGRLGKLGQGGQGGTTF 165  
  
QY 42 LCTEKSTANSYACKSIPKRLKVCREDYEDVWREIQIMHLSHHPNVRIKGTYESVVFH 101  
Db 166 LCVEKTTGKEFACKSIKRLTDEVEDVRRREIQIMHLSHHPNVISIKGAYEDVVAH 225  
  
QY 102 IYMEVCEGELFDRIVSKGHFSEREAVKILKITLGWVEACHSLGVMHRLDKPENFLFOSP 161  
Db 226 LVMECCAGGELFDRIQGHYTERKAAELTRTIQVGVVEACHSLGVMHRLDKPENFLFVSK 285  
  
QY 162 KDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILL 221  
Db 286 HEDSLKLTIDFGLSNFFKPPDDVFTDVGSPPYVAPEVLKCRKRGADVWSAGVILYILL 345  
  
QY 222 GVPFWAETESGIFRQILQGLKDFKSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCH 281  
Db 346 GVPFWAETESGIFRQILQGLKDFKSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCH 405

QY 282 PWIVDEQAPDKPLDPAVLSRLKQFSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDT 341  
Db 406 PWVQVGVAPDKPLDPAVLSRLKQFSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDT 465  
QY 342 DMSGTTTFEELKAGLKRVSGLMESEIKSLMDAADIDNSGTIDYGEFLAATLHNKMKERE 401  
Db 466 DKSGQITFEELKAGLKRVSGLMESEIKSLMDAADIDNSGTIDYGEFLAATLHNKMKERE 525  
QY 402 EILVAAPSDPKDGSYTTIDELQSACTEFLGCDTPLDDMIKEIDLDNDGKIDFSEPTAM 461  
Db 526 DHLFAAFTYFDKDGSGYITPDELQQAQCEBFGVEDVRIEELMRDQDNDGRIDYNEFAM 585  
QY 462 MRKGDGVGRSRTVMKMLNFNIA 483  
Db 586 MQKGSITGGPVKMGLEKSFSA 607  
  
RESULT 12  
T09940  
calcium-dependent protein kinase (EC 2.7.1.1) CDPK - pumpkin  
N:Alternate names: calcium-dependent calmodulin-independent protein kinase CDPK  
C:Species: Cucurbita pepo (pumpkin)  
C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 21-Jul-2000  
C:Accession: T09940  
R:Ellard-Ivey, M.; Hopkins, R.B.; White, T.J.; Lomax, T.L.  
Plant Mol. Biol. 39, 199-208, 1999  
A:Title: Cloning, expression and N-terminal myristoylation of CpCPK1, a calcium-depend  
A:Reference number: Z16898; MUID:99178773; PMID:10080688  
A:Accession: T09940  
A:Molecule type: mRNA  
A:Residues: 1-573 <ELL>  
A:Cross-references: EMBL:U90262; NID:G1899174; PIDN:AAB49984.1; PID:G1899175  
A:Experimental source: etiolated hypocotyls  
C:Genetics:  
C:Gene: CPK1  
C:Function:  
A:Description: serine/threonine-specific protein kinase activated by direct binding of  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein k;  
C:Keywords: ATP; calcium binding; EF hand; membrane protein; myristylation; phosphotrai  
F:108-368/Domain: protein kinase homology <KIN>  
F:447-479/Domain: calmodulin repeat homology <EFH>  
  
Query Match 65.9%; Score 1709.5; DB 2; Length 573;  
Best Local Similarity 64.8%; Pred. No. 8.3e-57;  
Matches 321; Conservative 78; Mismatches 79; Indels 17; Gaps 3;  
  
QY 4 KPNRP-----RP-----SNTVLPYQTPRLDRHYLLGKLGQGGQGGTTLCTEKS 47  
Db 72 KPEPPMEKVPVPMKRVSGSAGLRGGSVLQTKTGNFKEYYSLLGKLGQGGQGGTTCVCKA 131  
  
QY 48 TSANYACKSIPKRLKVCREDYEDVWREIQIMHLSHHPNVRIKGTYESVVFHIVMEYC 107  
Db 132 TGKEYACKSIKRLKVNEDVEDVRRREIQIMHLSHHPNVISIKGAYEDVAVAVQVMELC 191  
  
QY 108 EGGEFLDRIVSKGHFSEREAVKILKITLGWVEACHSLGVMHRLDKPENFLFVSKEESL 167  
Db 192 AGGELFDRILQGHYTERKAAELTRTIQVGVVEACHSLGVMHRLDKPENFLFVSKEESL 251  
  
QY 168 KATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLKCCYGPEDVWSAGVILYILLSGVPPFW 227  
Db 252 KTIDFGLSNFFKPGKFNVDVGSPPYVAPEVLKCRKRGADVWSAGVILYILLSGVPPFW 311  
  
QY 228 AETESGIFRQILQGLKDFKSDPWPPTSBAKDLIYKMLERSPKGRISAHEALCHPWVDE 287  
Db 312 AESSEGIFFEELHGLDLDFFSSDPWPSISDSAKDLVRRMLVRDPKRLTAYEVLCHPWVQD 371  
  
QY 288 QAAPDKPLDPAVLSRLKQFSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTI 347  
Db 372 GVADPKPLDPAVLSRLKQFSQWNKKKMLARVIAERLSEEEIGGLKELFKMIDTNSGTI 431  
QY 348 TFEELKAGLKRVSGLMESEIKSLMDAADIDNSGTIDYGEFLAATLHNKMKEREILVAA 407

Db 432 TFEELKAGLUKFGANUKESIEYDLMOQAADINDNGTTIDYGEFVAATLHLNKEIEKEDLLAA 491  
QY 408 FSDFOKDGSGYITIDELQACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDG 467  
Db 492 FSYFDKDGSGFITHDELQACKEFGIEDLQMEEMREVQNNDGSDYNEFVAMQKGVN 551  
QY 468 VGRSRTMMKNLNFNI 482  
Db 552 VNTGKKGLQS-SFSI 565

## RESULT 13

T05650  
calcium-dependent protein kinase (EC 2.7.1.1-) F20D10.350 - Arabidopsis thaliana  
N:Alternate names: protein F20D10.350  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 21-Jan-2000  
C:Accession: T05650  
R:Bevan, M.; Wedler, H.; Kutzner, M.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.  
submitted to the Protein Sequence Database, February 1999  
A:Reference number: Z15420  
A:Accession: T05650  
A:Molecule type: DNA  
A:Residues: 1-484 <BEV>  
A:Cross-references: EMBL:AL035538  
A:Experimental source: cultivar Columbia; BAC clone F20D10  
C:Genetics:  
A:Map position: 4  
A:Introns: 179/1; 227/1; 278/1; 316/3; 372/3; 447/3  
A:Note: F20D10.350  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific  
F:22-282/Domain: protein kinase homology <KIN>  
F:30-38/Region: protein kinase ATP-binding motif  
F:325-357/Domain: calmodulin repeat homology <EF1>  
F:361-393/Domain: calmodulin repeat homology <EF2>  
F:397-429/Domain: calmodulin repeat homology <EF3>  
F:431-463/Domain: calmodulin repeat homology <EF4>  
F:53/Active site: Lys #status predicted

Query Match 65.6%; Score 1700.5; DB 2; Length 484;  
Best Local Similarity 69.3%; Pred. No. 1.5e-56;  
Matches 325; Conservative 60; Mismatches 81; Indels 3; Gaps 2;

QY 14 VLPYQTPRLRDHYLLGKLGQOGQGTTLCTEKTSTANYACKSIPIKRLVCREDYEDVVR 73  
Db 12 VLQKQTPSIDRLDYLGLHKLGGQOGFTTYMCKEISTGREYACKSITKRLISKEDVEDVRR 71  
QY 74 EIQIMHLSSEHPNVRIKGTYESDVVHIVMEVCEGGELFDRIVSKGHFSEAEVKLTKT 133  
Db 72 EIQIMHLLAGYKNVITIKGAYEDPDYVHIVMELCSGGELFDRIIQRHYSERKAAELIKI 131  
QY 134 ILGVVEACHSLGVNHRDLKPENFLPDSPKDAAKLKATDGLSVFVKPGQYLDVVGSPY 193  
Db 132 IVGVVEACHSLGVNHRDLKPENFLVKNDDPSLKAIDGLSVFPKQIYEDVVGSPY 191  
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILOGKLDFKSPDPTI 253  
Db 192 VAPEVLLKHGPEADVWTAGVILYILVSGVPPFWAETQGGIFDAVLKGHIDFSDPWLJ 251  
QY 254 SEAKDLIYKMLERSPKRISAEALCHPWIVDEQAADPKLDPDAVLSRLKQFSOMNKK 313  
Db 252 SDSAKNLRGMLCSRPSRLTAHLVLRHPWTCENGAVAPDRALDPDAVLSRLKQFSAMNKK 311  
QY 314 KVALRVIAERLSEIEIGLKFQKIDTDNSGTTITFEELKAGLRKVGSELMESETKSLMD 373  
Db 312 QVALRVIAESLSEIEIAGLKEMFAMWTDNSGAIITFELKAGLRKYGTLTKDTEIRDJME 371  
QY 374 AADINDSGTIIDYGFLLAATLHNKMEREEILVAAPDFDKDGSYITIDELQSACTEFL 433  
Db 372 AADIDKSGTIIDYGFIAATIHLNKLREHLLSAFYPFDKDGSGYITIDELQHACAEQGM 431

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSRRTMMKNLNFNI 482  
Db 432 SDVFLEDVIKEVDQNDGRIDYGEFVAMQKGI-VG--RTMRKSINMSI 477

## RESULT 14

T02784  
calcium-dependent protein kinase (EC 2.7.1.1-) - maize (strain W64A)  
C:Species: Zea mays (maize)  
C:Date: 14-May-1999 #sequence\_revision 14-May-1999 #text\_change 16-Jun-2000  
C:Accession: T02784  
R:Murillo, I.; Jaeck, E.; Cordero, M.; San Segundo, B.  
submitted to the EMBL Data Library, July 1998  
A:Description: A calcium-dependent protein kinase possibly involved in pathogen defense  
sis-related PRms gene.  
A:Reference number: Z14736  
A:Accession: T02784  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-639 <MUR>  
A:Cross-references: EMBL:AJ007366; PIDN:CAA07481.1  
A:Experimental source: strain W64A; seed  
C:Function:

A:Description: probably involved in pathogen defense in maize plants  
C:Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kinase  
C:Keywords: ATP; calcium binding; EF hand; phosphotransferase; serine/threonine-specific;  
F:151-411/Domain: protein kinase homology <KIN>  
F:159-167/Region: protein kinase ATP-binding motif  
F:454-486/Domain: calmodulin repeat homology <EF1>  
F:490-522/Domain: calmodulin repeat homology <EF2>  
F:526-558/Domain: calmodulin repeat homology <EF3>  
F:560-592/Domain: calmodulin repeat homology <EF4>  
F:182/Active site: Lys #status predicted

Query Match 64.5%; Score 1672.5; DB 1; Length 639;  
Best Local Similarity 66.2%; Pred. No. 2.1e-55;  
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY 5 PNPR-RPS-----NTVLPYQTPRLRDHYLLGKLGQOGQGTTLCTEKTSTANY 52  
Db 120 PSPRPQVKRVSSAGLLGLSVLRRTKNTLKDYSLGRRLGQOGFTTHLCVERATGKEL 179  
QY 53 ACKSIPIKRLVCREDYEDVVRQIIMHLSSEHPNVRIKGTYESDVVHIVMEVCEGGEL 112  
Db 180 ACKSILKRLKLGSDDDVEDVRRQIIMHLLAGHPSVVGIRGAYEDI/VAVHLVWELCGGEL 239  
QY 113 FDRIVSKGHFSEAEVKLTKILGVVEACHSLGVNHRDLKPENFLPDSPKDAAKLKATDF 172  
Db 240 FDRIVRRGHYTERKAAELARVIVGYVEACHSMGVNHRDLKPENFLFADHSEEAALKTIDF 299  
QY 173 GLSVFVKPGQYLDVVGSPYVAPVPLKCKYGPETDVSAGVILYLLSGVPPFWAETES 232  
Db 300 GLSIFFRFGQIFTDVVGSPYVAPVPLKCKYGPEDVWSAGVILYLLSGVPPFWAENRQ 359  
QY 233 GIFRQILOGKLDFKSDPMTTISEAAKDLIYKMLERSPKRISAEALCHPWIVDEQAAPD 292  
Db 360 GIFEVLHGLRDFSEPEWPSISDGAKOLVRRLVDRPKRLTAHEVLVRHPWVQGVGVPAD 419  
QY 293 KPLDPAVLSRLKQFSOMNKKIIMKALRVIAERLSEIEIGLKFQKIDTDNSGTTITFEEL 352  
Db 420 RPLDSAVLSRMKQFSAMNKKIIMKALRVIAERLSEIEIGLKFQKIDTDNSGTTITFEEL 479  
QY 353 KAGLRKVGSELMESEIEIKSLMDAADIIDNSGTTIDYGEFLLAATLHNKMEREEILVAAPSD 412  
Db 480 KVGLEKVGANLQSEIEIYALMQAADVNNNGTTIDYGEFTIAATLHLNKVEREDHLFAAFQYFD 539  
QY 413 KDGSGYITIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVRSR 472  
Db 540 KDGSGYITADELQVACEFGLGVDQLEDLGEVDQNDGRIDYNEFVAMQK-PTVGGSR 598

RESULT 15  
H84810

probable calcium-dependent protein kinase [imported] - Arabidopsis thaliana  
C;Species: Arabidopsis thaliana (mouse-ear cress)  
C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Mar-2001  
C;Accession: H84810  
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A;Reference number: A84420; MUID:20083487; PMID:10617197  
A;Accession: H84810  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-583 <STO>  
A;Cross-references: GB:AE002093; NID:g3928078; PIDN:AAC79604.1; GSPDB:GN00139  
C;Genetics:  
A;Gene: At2g38910  
A;Map position: 2  
C;Superfamily: calcium-dependent protein kinase; calmodulin repeat homology; protein kin  
C;Keywords: EF hand

Query Match	63.3%	Score	1640.5	DB 2	Length	583
Best Local Similarity	66.9%	Pred. No.	3e-54			
Matches	307	Conservative	67	Mismatches	84	Indels 1; Gaps 1;
QY	12	NTVLPYQTPRLRDHYLLGKXGQGFQTTYLCTEKSTANSYACKSIPKRLVCREDEYDV	71			
Db	120	DSVLGRKTNLKDIIYSVGRKLGQGFQTTFLCVDDKTKGFEACKTIKRKLTTTPEDVEDV	179			
QY	72	WREIQIMHLSHPNVIRIKGTVEDSVFVHIMEVCEGGELEFDRIVSKGHFSEREAVKLI	131			
Db	180	RREIQIMHLSHPNVIQIVGAYEDAVAVHVNVEICAGGELEFDRIRIQRGHYTEKAAELA	239			
QY	132	KTILGVVEACHSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGCOYLYDVVGSP	191			
Db	240	RIIVGVIEACHSLGVNHRDLKPNFLFVSGDEEAALKTIDFGLSVFPKGETFDVVGSP	299			
QY	192	YVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQIQKLDLDFKSDPWP	251			
Db	300	YVVAPEVLRKHYSHECDVMSAGVILYLLSGVPPFWDETEQGIQEQVLKGLDLDIFSEPPW	359			
QY	252	TISEAAKDLIYKMLRSPKKRISAEALCHPWIVDQAAAPDKPLDPAVLRLKQFSQMNK	311			
Db	360	SVSESADLVRRMLIRDPKKRMTTHEVLCHPWAVDGVADLKDPLDSAVLSRLQQFSAMNK	419			
QY	312	IKQMALRVIAERLSEEEIGGLKELFKMIDTNSGTTTFBELKAGLRKRVGSELMESEIKSL	371			
Db	420	LKKIAIKVIAESLSEEEIAGLKEMFKMIDTNSGHITLLELKKGLDRVGADLKDSILGL	479			
QY	372	MDAADIDNSGTTIDYGEFLAATLHMKNKREERILVAAFSDFKDGSYITIDELQSACTEF	431			
Db	480	MQAADIDNSGTTIDYGEFIAAMVHNLKIEKEDHLFTAFSYFDQDGSYITRDELQQAQKQF	539			
QY	432	GLCDTFLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGR	470			
Db	540	GLADVHLDDILREVVDKNDGRIDYSEFVDM-QDTGFGK	577			

Search completed: November 28, 2003, 10:36:20  
Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 24 Seconds

(without alignments)  
969.926 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPYQTP.....KMLNFIADAFGVGDEKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1944	75.0	508	1	CDPK SOYBN
2	1724	66.5	610	1	CDP1_ARATH
3	1586	61.2	542	1	CDP2_ORYZA
4	1482	57.2	533	1	CDP2_ORYZA
5	1460.5	56.3	513	1	CDP2_MAIZE
6	1460	56.3	534	1	CDP1_ORYZA
7	1432.5	55.2	532	1	CDPK_DAUCA
8	854	32.9	602	1	CRK_DAUCA
9	591	22.8	499	1	KCCD_HUMAN
10	589.5	22.7	374	1	KCCD_MOUSE
11	589.5	22.7	374	1	KCC1_RAT
12	587.5	22.7	370	1	KCC1_HUMAN
13	578.5	22.3	473	1	KCC4_HUMAN
14	574.5	22.2	533	1	KCCD_RAT
15	574	22.1	469	1	KCC4_MOUSE
16	572	22.1	474	1	KCC4_RAT
17	571.5	22.0	542	1	KCCB_MOUSE
18	569.5	22.0	542	1	KCCB_RAT
19	567.5	21.9	478	1	KCCA_HUMAN
20	566.5	21.8	664	1	KCCB_HUMAN
21	565.5	21.7	478	1	KCCA_RAT
22	549.5	21.2	478	1	KCCA_MOUSE
23	544.5	21.0	529	1	KCCG_MOUSE
24	543.5	21.0	472	1	KCCG_HUMAN
25	539	20.8	527	1	KCCG_RAT
26	534.5	20.6	424	1	KPSH_HUMAN
27	533.5	20.6	386	1	KPBG_HUMAN
28	532.5	20.5	386	1	KPBG_RAT
29	526	20.3	387	1	KPBG_MOUSE
30	524.5	20.2	387	1	KPBG_MOUSE
31	514.5	19.8	295	1	KMLC_DICDI
32	509	19.6	1431	1	DAPK_HUMAN
33	505	19.5	433	1	CDK1_RAT

34	505	19.5	740	1	CDK1_HUMAN
35	505	19.5	756	1	CDK1_MOUSE
36	499	19.2	335	1	KCC1_SCHPO
37	489.5	18.9	752	1	KGAA_CHICK
38	486	18.7	735	1	KGAA_RAT
39	484.5	18.7	512	1	K110_ARATH
40	482.5	18.6	733	1	K6A2_HUMAN
41	481	18.5	724	1	K6A1_MOUSE
42	480	18.5	735	1	K6A1_HUMAN
43	479	18.5	546	1	CHK2_MOUSE
44	477	18.4	733	1	K6AA_XENLA
45	476.5	18.4	733	1	K6AA_MOUSE

## ALIGNMENTS

### RESULT 1

CDPK\_SOYBN

ID CDPK SOYBN STANDARD; PRT; 508 AA.

AC P28583;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-DEC-1992 (Rel. 24, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcium-dependent protein kinase SK5 (EC 2.7.1.1) (CDPK).

OS Glycine max (Soybean).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.

ON NCBI\_TaxID=3847;

RX STRAIN=cv. Williams;

RX MEDLINE=91240279; PubMed=1852075;

RA Harper J.F., Sussman M.R., Schaller G.E., Putnam-Evans C.,

RA Charbonneau H., Harmon A.C.;

RT "A calcium-dependent protein kinase with a regulatory domain similar

RT to calmodulin."

RL Science 252:951-954 (1991)

CC -! FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT

CC INVOLVE CALCIUM AS A SECOND MESSENGER.

CC -! ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY

CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

CC -! TISSUE SPECIFICITY: FOUND THROUGHOUT THE PLANT.

CC -! MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN SOYBEAN.

CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CAMK SUBFAMILY.

CC -! SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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CC EMBL: M64987; AAB00806.1; -

CC PIR: A43713; A43713.

CC HSSP: Q63450; 1A06.

CC InterPro: IPR002048; EF-hand.

CC InterPro: IPR000719; Prot\_kinase.

CC InterPro: IPR002290; Ser\_thr\_kinase.

CC Pfam: PF00036; ehand; 4.

CC Pfam: PF00069; pkinase; 1.

CC ProDom: PD000012; EF-hand; 2.

CC ProDom: PD000001; Prot\_kinase; 1.

CC SMART: SM00054; EFh\_4\_TKc; 1.

CC PROSITE: PS00018; EF\_HAND; 4.

CC PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

CC PROSITE: PS0108; PROTEIN\_KINASE\_ST; 1.

CC PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.

KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Calcium-binding; Phosphorylation.
KW	DOMAIN 34 292 PROTEIN KINASE
FT	NP_BIND 48 ATP (BY SIMILARITY)
FT	BINDING 63 ATP (BY SIMILARITY)
FT	ACT_SITE 158 BY SIMILARITY
FT	CA_BIND 348 EF-HAND 1 (POTENTIAL)
FT	CA_BIND 384 EF-HAND 2 (POTENTIAL)
FT	CA_BIND 420 EF-HAND 3 (POTENTIAL)
FT	CA_BIND 454 EF-HAND 4 (POTENTIAL)
SQ	SEQUENCE 508 AA; 57169 MW; AFCD5122419284 CRC64;
Query Match	
Best Local Similarity 75.0%; Score 1944; DB 1; Length 508;	
Matches 370; Conservative 51; Mismatches 51; Indels 4; Gaps 3;	
QY	14 VLPVQTPRLRDHYLGGKGGQGGTTLCTESTSANYACKSIPKRLKVCREDYEDVWR 73
DB	22 VLPQTNIREVVEVGRKGGQGGTTFCTRASGGKGFACKSIPKRLKCKEDYEDVWR 81
QY	74 EIQIMHLSHPNVVRIKGTYESVFIHVEVCEGGELEFDRIVSKGHFSEREAVKLKT 133
DB	82 EIQIMHLSHPNVVRIEGYEDSTAVHLMVCEGGELEFDRIVQKGYHSEQAARLKT 141
QY	134 ILGVEACHSLGVMHRLDKPENLFDSPKDDAKLKATDFGLSVFKPGQYLYDVVGSPPY 193
DB	142 IVEVVEACHSLGVMHRLDKPENLFDIDEDAKLKATDFGLSVFKPGESFCDDVGSPPY 201
QY	194 VAPEVLKCKVGPEDVWSAGVILYLLSGVPPFAETESIFRQILGKLDKDFSDPWTI 253
DB	202 VAPEVLKCKVGPEDVWSAGVILYLLSGVPPFAETESIFRQILGKLDKDFSDPWTI 261
QY	254 SEAAKLIYKWLSPKRRISAHEALCHPWIVDEQAAPDKPLDPAPVLSRLKQFSQNMKIK 313
DB	262 SDSAKDLIRKWLQNPTRTLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSQNMKIK 321
QY	314 KMAIRVIAERLSSEETGGELKELFMIDTNSGTTITFEELKAGLKRVSSELMSEIISLMD 373
DB	322 KMAIRVIAERLSSEETGGELKELFMIDTNSGTTITFEELKAGLKRVSSELMSEIISLMD 381
QY	374 AADIDNSGTTIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSGYITIDELQACATERGL 433
DB	382 AADIDNSGTTIDYGEFLAATVHLNKLREENVLSAFSFDKDGSGYITIDELQACATERGL 441
QY	434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMRKGD- GVGSRSTMMKNLNFNIADAFV 488
DB	442 DDIHIDMIKEIDQDNDGQIDYGEFAAMRKGGIGR-RTMRKTL--NLRDALGL 494
RESULT 2	
ID	CDPI_ARATH STANDARD; PRT; 610 AA.
AC	Q06850;
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DE	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Calcium-dependent protein kinase, isoform AK1 (EC 2.7.1.-) (CDPK).
GN	AK1 OR AR5G04870 OR MUK11.19.
OS	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC	Spekmatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.
OX	NCBI_TaxID=3702;
RN	(1)
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Columbia;
RX	MEDLINE=93213795; PubMed=7916621;
RA	Harper J.F., Binder B.M., Sussman M.R.;
RT	"Calcium and lipid regulation of an Arabidopsis protein kinase
RT	expressed in Escherichia coli.";
RL	Biochemistry 32:3282-3290(1993).
RN	(2)
RP	SEQUENCE FROM N.A.
RC	STRAIN=cv. Columbia;
RX	MEDLINE=98162728; PubMed=9501997;
RA	Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA	Tabata S.;
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT	Sequence features of the regions of 1,191,918 bp covered by seventeen
RT	physically assigned P1 clones.";
RL	DNA Res. 4:401-414(1997).
CC	-1- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC	INVOLVE CALCIUM AS A SECOND MESSENGER.
CC	-1- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY
CC	PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC	-1- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN MOUSE-EAR
CC	CRESS.
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC	CAMK SUBFAMILY.
CC	-1- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
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CC	OR SEND AN EMAIL TO LICENSE@ISB-SIB.CH).
CC	EMBL; L14771; AAA32761.1; --
DR	EMBL; AB008271; BAB08991.1; --
DR	PIR; A49082; A49082.
DR	HSSP; P02588; 1PON.
DR	InterPro; IPR002048; EF-hand.
DR	InterPro; IPR000719; Prot kinase.
DR	InterPro; IPR002290; Ser Thr_pkinase.
DR	Pfam; PF00036; ehand; 4.
DR	Pfam; PF00069; pkinase; 1.
DR	ProDom; PD000012; EF-hand; 2.
DR	ProDom; PD000001; Prot kinase; 1.
DR	SMART; SM00054; Eph; 4.
DR	SMART; SM00220; S_TKc; 1.
DR	PROSITE; PS00018; EF_HAND; 4.
DR	PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR	PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR	PROSITE; PS00011; PROTEIN KINASE DOM; 1.
KW	Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW	Calcium-binding; Phosphorylation; Multigene family.
FT	DOMAIN 150 408 PROTEIN KINASE
FT	NP_BIND 156 164 ATP (BY SIMILARITY)
FT	BINDING 179 179 ATP (BY SIMILARITY)
FT	ACT_SITE 274 274 BY SIMILARITY
FT	CA_BIND 464 475 EF-HAND 1 (POTENTIAL)
FT	CA_BIND 500 511 EF-HAND 2 (POTENTIAL)
FT	CA_BIND 536 547 EF-HAND 3 (POTENTIAL)
FT	CA_BIND 570 581 EF-HAND 4 (POTENTIAL)
SQ	SEQUENCE 610 AA; 68253 MW; 41868DF12B0DF9FB CRC64;
Query Match	
Best Local Similarity 66.5%; Score 1724; DB 1; Length 610;	
Matches 329; Conservative 62; Mismatches 91; Indels 20; Gaps 2;	
QY	2 ETKP-----NRRP-----SNTVLPYQTPRLRDHYLGGKGGQGGTTY 41
DB	106 ETKPESKDPDPKPKPKMKRVSSAGLRTESVLQRTKTFEFYSLGRKLGQGGTTF 165
QY	42 LCTEKSTANYACKSIPKRLKVCREDYEDVWEIQLMHLSHPNVVRIKGTYESVFWH 101
DB	166 LCVEKTTGKFAKSIARKKLLTDEVEDVREIQLMHLAGHPNVISIKGAYEDVVAHV 225
QY	102 IVMVECEGGELEFDRIVSKGHFSEREAVKLKTLGVWEACHSLGVMHRLDKPENLFDSP 161
DB	226 LWMECCAGGELEFDRIIQRGHYTERKAAELTRIVGVWEACHSLGVMHRLDKPENLFDSP 285
QY	162 KDDAKLKATDFGLSVFKPGQYLYDVVGSPPYVAPEVLKCKYGPEDVWSAGVILYLLS 221

Db 286 HEDSLKTTIDFGLSMFFKDDVFTDVVGSPPYVAPEVLRRKRYGPEADVMSAGVIVVILLS 345  
Qy 222 GVPPFWAETESGIFRLOLQKLDKSDPMTTSEAAKDLIYKMLERSPKKRISAHEALCH 281  
Db 346 GVPPFWAETEQGIFEGVLGDDJDFSSDPWPSISAKDLVRKMLVRDPKRLTAHQVLCH 405  
Qy 282 PWIVDEQAAPDPLDPAVLRLKQFSQMNKIKKMARLVIAERLSEEEIGGLKELFQVMDT 341  
Db 406 PWVQDGVAPDKPLDSAVLSRMKQFSAMNKKFKMARLVIAERLSEEEIAGLKEMFNWIDA 465  
Qy 342 DNSGTTTFELKAGLKRVSSELMESIKSLMDAADTNSGTTDYGFLAATLHMNQERE 401  
Db 466 DKSQGITFELKAGLKRVSSELMESIKSLMDAADTNSGTTDYGFLAATLHMNQERE 525  
Qy 402 EILVAAFSDFDKGSGYITIDELQSACTEFGLCDDTPLDDMIKEIDLDNGKIDSEFTAM 461  
Db 526 DHLFAAFTYFDKSGSYITPDELQACEEFGVEDVRIELMRDVOQDNGRIDYNEFVAM 585  
Qy 462 MRKGDGVRSTRMKNLNFNIA 483  
Db 586 MQKGSITGGPVKMGLEKFSIA 607

## RESULT 3

CDP3\_ORYSA  
ID CDP3\_ORYSA STANDARD; PRT; 542 AA.  
AC P53684;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Calcium-dependent protein kinase, isoform 11 (EC 2.7.1.-) (CDPK 11).  
OS CPK11.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Arborio; TISSUE=Coleoptile;  
RX MEDLINE=95284352; PubMed=7766885;  
RA Breviario D., Morello L., Giani S.;  
RT "Molecular cloning of two novel rice cDNA sequences encoding putative  
calcium-dependent protein kinases";  
RL Plant Mol. Biol. 27:953-967(1995).  
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT  
INVOLVE CALCIUM AS A SECOND MESSENGER.  
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).  
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC CAMK SUBFAMILY.  
CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL; X81393; CAA57156.1; -.  
DR PIR; S56651; S56651.  
DR HSP; Q63450; 1A06.  
DR Gramene; P53684; -.  
DR InterPro; IPR002048; EF-hand.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR Pfam; PF00036; ehand; 4.  
DR Pfam; PF00069; pkinase; 1.  
DR ProDom; PD000012; EF-hand; 2.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00054; Eph; 3.

SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00018; EF\_HAND; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Calcium-binding; Phosphorylation; Multigene family.  
FT DOMAIN 79 337 PROTEIN KINASE.  
FT NP\_BIND 81 89 ATP (BY SIMILARITY).  
FT BINDING 108 108 ATP (BY SIMILARITY).  
FT ACT\_SITE 202 202 BY SIMILARITY.  
FT DOMAIN 393 404 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).  
FT DOMAIN 429 440 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).  
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).  
FT CA\_BIND 499 510 EF-HAND 4 (POTENTIAL).  
SQ SEQUENCE 542 AA; 61166 MW; D4D257275C126DDA CRC64;  
Query Match 61.2%; Score 1586; DB 1; Length 542;  
Best Local Similarity 63.9%; Pred. No. 5.6e-73;  
Matches 304; Conservative 68; Mismatches 102; Indels 2; Gaps 2;  
Qy 11 SNTVLPTQPLRLDRHYLLGKLGQGFQGTTLCTEKSSTANYACKSIKPKKLVCREDDYED 70  
Db 64 SINLGRKTADREHYIIGRKLGGQAFQGTTLCTEINTGEYACKTIPKRLKITKEDVED 123  
Qy 71 VVREIQIMHLSHHPNVVRIKGTIEDSVFVHVMVEGEGELFDRIVSKGHSEAEVKL 130  
Db 124 VVREIQIMHLSGHKNVVAIKDYEDGQAVHVMELCAGGELFDRIOEKGHYSERAAEL 183  
Qy 131 INTILGVVACHSLGVMHRLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQYLYDVVGS 190  
Db 184 IRIIVSIAMCHSLGVMHRLKPNFLFLDLDKDDLSIKKIDFGLSVFYKPGQYLYDVVGS 243  
Qy 191 PYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFAETESGIFRLOLQKLDKSDPW 250  
Db 244 PYVAPEVLKRYGPESDVMSAGVILYLLSGVPPFAETQGGIFDAVLKGHIDFQSDPW 303  
Qy 251 PTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQMN 310  
Db 304 PKISDSAKDLIRKMLSHCPSERLKAHEVLRHWPICENGVAATQALDPSVISRLKQFSAMN 363  
Qy 311 KIKKMARLVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMESIEKS 370  
Db 364 KLKLLARLVIAERLSEEEIAGLRNFKAVDTKNRGVITFELREGULRRFGAEFKDTEIGD 423  
Qy 371 LMDAADTNSGTTDYGFLAATLHMNQEREELVAAFSDFDKGSGYITIDELQSACTE 430  
Db 424 IMEAAHNNNNVTIHYEEFIAATPLNKIEREHLAAFTYFDKQSGSYITVDKLRACGE 483  
Qy 431 FGLCDTPLDDMIKEIDLDNGKIDSEFTAMMRKRGDVGGRS-RTMMKNLNFNIA 485  
Db 484 HNMEDSLJEEIISVEDQNDGQIDYAEFVAMM-QQSNVGLGHWQTMESLNLVALRDA 538  
RESULT 4  
CDP2\_ORYSA  
ID CDP2\_ORYSA STANDARD; PRT; 533 AA.  
AC P53683;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Calcium-dependent protein kinase, isoform 2 (EC 2.7.1.-) (CDPK 2).  
GN CPK2.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Arborio; TISSUE=Coleoptile;  
RX MEDLINE=95284352; PubMed=7766885;  
RA Breviario D., Morello L., Giani S.;  
RT "Molecular cloning of two novel rice cDNA sequences encoding putative







```

FT CA_BIND 379 390 EF-HAND 1 (POTENTIAL)
FT CA_BIND 415 426 EF-HAND 2 (POTENTIAL)
FT CA_BIND 451 462 EF-HAND 3 (POTENTIAL)
FT CA_BIND 486 497 EF-HAND 4 (POTENTIAL)
SQ SEQUENCE 513 AA; 58081 MW; 235A61630C0AC336 CRC64;

Query Match 56.3%; Score 1460.5; DB 1; Length 513;
Best Local Similarity 60.0%; Pred. No. 1e-66;
Matches 276; Conservative 78; Mismatches 105; Indels 1; Gaps 1;

QY 7 PRPNTVLPYQTPRLDRHLLGKLGQGFQGTTLCTEKTSTANYACKSIKPKLVCRE 66
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 46 KPXTADTILGQYEDVRSYSGELGRGQFGVTVLCTEIASGRQVACKSIKRLVSKA 105
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 67 DYEDVMREIQIMHLSHPNVRIRKTYEDSVFVHVMVEVCEGGEFDRIVSKGHFSERE 126
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 106 DREDIRREIQIMHLSGQPNIVEPRGAYEDKSNVHVMELCAGGELFDRIIAKHGYTERA 165
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 127 AVKLKTLGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDGLSVFVKQOYLYD 186
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 166 AATICRAVNVVNIHFVGWVHRDLKPNFLATMEENAMLKATDGLSVFTEEGMYRD 225
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 187 VVGSPYVVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDPK 246
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 226 IVGSAYVAPVLRISYCKEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDPK 285
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 247 SDPWTISEAKDLIYKMLERSPKKRSIAHEALCHPWIVDQAPKPLDPAVLRLKQF 306
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 286 SQPWPSISEAKDLVRLKMLTRDPKRLTSAQVLOHQLREGCEASDKPDSAVLSRMKQF 345
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 307 SOMNKKIKMARLVTAERLSSEIEGKLEFKYMDTNSGTTTFELKAGLRKRVGSELMES 366
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 346 RAMNKKIKMARLVTAERLSSEIEGKLEFKYMDTNSGTTTFELKAGLRKRVGSELMES 405
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 367 EIKSLMDAADIDNSGTTIDYGFLLAATLHMKNKEREILVAAFSDPKDGGSVITIDELQS 426
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 406 EVKQLMEADVDGSGIDYVEFIATMRHKLDERDEHLFKAFQYFDKNSGFIITRDELES 465
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 427 ACTFGLGCDT-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 466 ALIEHEMGDTSTIREIIEVTDNDGRINVEFCAMMRGG 505

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## RESULT 6

```

CDPI_ORYSA
ID_CDP1_ORYSA STANDARD; PRT; 534 AA.
AC PS3682;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Calcium-dependent protein kinase, isoform 1 (EC 2.7.1.-) (CDPK 1).
GN SPK.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=93314961; PubMed=8325505;
RA Kawasaki T., Hayashida N., Baba T., Shinozaki K., Shimada H.;
RT "The gene encoding a calcium-dependent protein kinase located near
RT the sh1 gene encoding starch branching enzyme 1 is specifically
RL expressed in developing rice seeds.";
RL Gene 129:183-189(1993).
CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT
CC INVOLVE CALCIUM AS A SECOND MESSENGER.
CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM (BY SIMILARITY).
CC -!- DEVELOPMENTAL STAGE: SPECIFICALLY EXPRESSED IN SEEDS.
CC -!- MISCELLANEOUS: THERE ARE MULTIPLE CDPK ISOFORMS IN RICE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.

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CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.
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CC EMBL: D13436; BAA02698.1; -.
DR PIR: JCI515; JCI515.
DR HSSP: P02593; ICDM.
DR Gramene: P53682; -.
DR InterPro: IPR002048; EF-hand.
DR InterPro: IPR000719; Prot.Kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR Pfam: PF00036; ehand; 4.
DR ProDom: PD000012; EF-hand; 2.
DR ProDom: PD000001; Prot.kinase; 1.
DR SMART: SM00054; EFh_2; -.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00018; EF HAND; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS00108; PROTEIN KINASE ST; 1.
DR PROSITE: PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding,
KW Calcium-binding; Phosphorylation; Multigene family.
FT DOMAIN 73 331 PROTEIN KINASE.
FT NP_BIND 79 87 ATP (BY SIMILARITY).
FT BINDING 102 102 ATP (BY SIMILARITY).
FT ACT_SITE 197 197 BY SIMILARITY.
FT DOMAIN 387 398 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 422 432 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 457 468 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT CA_BIND 491 502 EF-HAND 4 (POTENTIAL).
SQ SEQUENCE 534 AA; 60573 MW; 1932CCD2C4F8C5 CRC64;

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Query Match 56.3%; Score 1460; DB 1; Length 534;
Best Local Similarity 59.2%; Pred. No. 1.e-66;
Matches 280; Conservative 84; Mismatches 105; Indels 4; Gaps 4;

QY 14 VLPYQTPRLDRHLLGKLGQGFQGTTLCTEKTSTANYACKSIKPKLVCREYDVMR 73
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 VLGYKTPNRELYTLGRELGGQFGKTYLCTEISTGCOYACKTILKSNLRCVSDIEDVRR 120
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 74 EIQIMHLSHPNVRIRKTYEDSVFVHVMVEVCEGGEFDRIVSKGHFSEREAVKLK 133
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 EIQIMHLSGQKNIVTITKTYEDEQAVHVMELCAGGELFSKIQKRGHYSERKAAELIKI 180
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 134 ILGVVEACHSLGVNHRDLKPNFLDPSKDDAKLKATDGLSVFVKQOYLYDVVGSPPY 193
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 181 IVGIETCHSGVNHRLKPNFLDADDEFVSKAIDFGLSVFRPQGVFREVVGSPYY 240
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDPKDPWPTI 253
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 241 IAPVLEKRYGPEADIWTAGVILYLLTGVPPFWADTQSGIYKVLGDRIDFKNNRPRI 300
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 254 SEAAKDLIYKMLERSPKKRSIAHEALCHPWIVDQAPKPLDPAVLRLKQFSQMNKIK 313
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 301 SDSAKDLIKMLCPYPLERLKAHEVLKHPWICDNGVATNRALDPSVLPRLKQFSAMNRLK 360
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 314 KMALRVTAERLSSEIEGKLEFKYMDTNSGTTTFELKAGLRKRVGSELMESIKSLMD 373
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 361 KLSLQIIAERLSSEIEVGLREMFKAMDTKRNSVVVTFGLK-GLKRYSSVFKDTINDLME 419
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 374 AADINDSGTIDYGEFLAATLHMKNKEREILVAAFSDPKDGGSVITIDELQSACTEFLG 433
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 420 AAD-DITSTINWEEFAAAVSLNKIEREKHLMFAFTYFDKGGFTIYDVKLQKACMRNM 478
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKG-DVGRSRTMMKNLNFNIADA 485
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Db 479 EDTFLEEMILEVDQNNDGQIDYAEFVTMMQSNFGLG-WQTVESSLNVALREA 530

## RESULT 7

CDPK DAUCA STANDARD; PRT; 532 AA.

ID CDPK DAUCA PRT; 532 AA.

AC P28582;

DT 01-DEC-1992 (Rel. 24, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcium-dependent protein kinase (EC 2.7.1.-) (CDPK).

OS Daucus carota (Carrot)

OC Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; campanulids; Apiales; Apiaceae; Daucus.

OX NCBI\_TaxID=4039;

XX [1]

RN SEQUENCE FROM N.A.

RP Choi J.H.;

RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.

RL [2]

RN SEQUENCE OF 108-532 FROM N.A.

RX MEDLINE=92003674; PubMed=1912486;

RT Sven K.-L., Choi J.H.;

RT "Isolation and sequence analysis of a cDNA clone for a carrot

RT calcium-dependent protein kinase: homology to

RT calcium/calmodulin-dependent protein kinases and to calmodulin.";

RL Plant Mol. Biol. 17:581-590(1991).

CC -!- FUNCTION: MAY PLAY A ROLE IN SIGNAL TRANSDUCTION PATHWAYS THAT

CC INVOLVE CALCIUM AS A SECOND MESSENGER.

CC -!- ENZYME REGULATION: ACTIVATED BY CALCIUM. AUTOPHOSPHORYLATION MAY

CC PLAY AN IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC CAMK SUBFAMILY.

CC -!- SIMILARITY: Contains 4 EF-hand calcium-binding domains.

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DR EMBL; X56599; CAA39936.1; --

DR PIR; S17759; S17759.

DR PIR; T14335; T14335.

DR HSP; Q63450; IA06.

DR InterPro; IPR002048; EF-hand.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_kinase.

DR Pfam; PF00036; pfkinase; 4.

DR Pfam; PF00069; pkinae; 1.

DR ProDom; PD000012; EF-hand; 2.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00054; EFh; 4.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00018; EF\_HAND; 4.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

KW Transferase: Serine/threonine-protein kinase; ATP-binding;

KW Calcium-binding; Phosphorylation.

FT DOMAIN 81 339 PROTEIN KINASE.

FT NP\_BIND 87 95 ATP (BY SIMILARITY).

FT BINDING 110 110 ATP (BY SIMILARITY).

FT ACT\_SITE 205 205 BY SIMILARITY.

FT CA\_BIND 395 406 EF-HAND 1 (POTENTIAL).

FT CA\_BIND 431 442 EF-HAND 2 (POTENTIAL).

FT CA\_BIND 465 476 EF-HAND 3 (POTENTIAL).

FT CA\_BIND 500 511 EF-HAND 4 (POTENTIAL).

SEQUENCE 532 AA; 60065 MW; F03B6F036A0AE348 CRC64;

SQL

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DR PIR: S60052; S60052.
DR HSSP; Q63450; 1A06.
DR InterPro; IPR002048; EF-hand.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR002290; Ser Thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Repeat.
FT DOMAIN 20 40 3 X 7 AA TANDEM REPEATS OF S-[LI]-P-X-X-
FT D-X.
FT REPEAT 20 26 1.
FT REPEAT 27 33 2.
FT REPEAT 34 40 3.
FT DOMAIN 148 410 PROTEIN KINASE.
FT NP_BIND 154 162 ATP (BY SIMILARITY).
FT BINDING 180 180 ATP (BY SIMILARITY).
FT ACT_SITE 276 276 BY SIMILARITY.
FT DOMAIN 465 476 ANCESTRAL CALCIUM SITE 1 (POTENTIAL).
FT DOMAIN 502 513 ANCESTRAL CALCIUM SITE 2 (POTENTIAL).
FT DOMAIN 542 553 ANCESTRAL CALCIUM SITE 3 (POTENTIAL).
FT DOMAIN 574 585 ANCESTRAL CALCIUM SITE 4 (POTENTIAL).
FT SEQUENCE 602 AA; 67184 MW; 1D10BF68B37BF447 CRC64;
SQ
Query Match 32.9%; Score 854; DB 1; Length 602;
Best Local Similarity 41.2%; Pred. No. 3.2e-36;
Matches 184; Conservative 90; Mismatches 155; Indels 18; Gaps 8;
QY 28 LCKKLGGOGFGTYLCTEKSTSNY-----ACKSIKPKLKVREDYEDVWREIQIMHLS 82
DB 150 VGEVGRGHFG--YTCRAKFKGFKGQDVAVKVIPIKAKMTAIAIEDVRREVKILRALT 207
QY 83 EHPNVVRIRKGTVEDSVFVHVMVEVCCEGELFRIVSK-GHFSEREAVKLITLGVVEAC 141
DB 208 GHNNLVQFYDAEDHTNIVVMWELCEGELLRLSRGKYTEDDKAKVMIOILNVVAF 267
QY 142 HSLGVNHRDLKPENFLDPSKDAKLKATDFGLSVFKPGQYLYDVGVGPPYVVAPEVLKK 201
DB 268 HLQGVVHRDLKPENFLFKSKEDSQLKATDFGLSDYVKVDFERLNDIVGSAIVAEVLHR 327
QY 202 CYGPEIDVWSAGVILYLLSGVPPFAETESGIFROILOGLKDFKSDPMTTISEAKOLI 261
DB 328 SYSTADVMSIGVISYLLCGSRPFWARTESGIFRAVLKANLSFDEPPWPVSSEAKDFV 387
QY 262 YKMLERSPKKRISAEALCHPWIVDEQAAPDKPLPAVLRLKQFSQNMKIKKMLALRVIA 321
DB 388 KELLNKDPRKRTAAQALCHSWIKNSNDI-KFPLDILVFLMKVYMRSSPLRAALRLS 446
QY 322 ERLSEEEIGGLKELFMIDTNSGTTITFEELKAGLKRVGSELM-ESEIKSLMDAADIDNS 380
DB 447 KTLTVDELFLYKEQVLEPTKNGTISLENIKQALMRNSTDAKDSRVLDDLVSINALQY 506
QY 381 GTIDYGEFLAATLHNKMER-----EELLVAASDFDKGSGVITIDELQSACTEFLGDT 436
DB 507 RMDFEEFCAALSVHQHEALDRWQHARCAVDLFEKQGNRAIMTEELAS---ELGLGFS 563
QY 437 -PLDDMIKEILDNDGKIDFSFTAMM 462
DB 564 IPVHAVLHDWIRHTDGKLSFLGYVKLL 590
RESULT 9
ID KCED HUMAN STANDARD; PRT; 499 AA.
AC Q13557; O9UGH6; O9UC09;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type II delta chain

```

```

DE DE (EC 2.7.1.123) (CaM-kinase II delta chain) (CaM kinase II delta
DE subunit) (CaMK-II delta subunit).
DE CAMK2D.
GN Homo sapiens (Human).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP TISSUE=Myocardium;
RX MEDLINE=99205154; PubMed=10189359;
RA Hoch B., Meyer R., Hetzer R., Krause E.-G., Karczewski P.;
RT "Identification and expression of delta-isoforms of the
RT multifunctional Ca2+/calmodulin-dependent protein kinase in failing
RT and nonfailing human myocardium.";
RT Circ. Res. 84:713-721(1999).
RN [2]
RN SEQUENCE OF 1-243 FROM N.A.
RP TISSUE=Insulinoma;
RC Rochlitz H., Voigt A., Lankat-Buttgerit B., Goeke B., Heimberg H.,
RA Nauck M.A., Schlemann U., Schatz H., Pfeiffer A.;
RT "Cloning of the human calcium/calmodulin dependent protein kinase II
RT isoforms in human beta cells.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE OF 302-417 FROM N.A.
RX MEDLINE=97214619; PubMed=9060999;
RA Tombes R.M., Krystal G.W.;
RT "Identification of novel human tumor cell-specific CaMK-II variants.";
RL Biochim. Biophys. Acta 1355:281-292(1997).
CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN
CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.
CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,
CC AND DELTA.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=6;
CC Name=Delta 2;
CC IsoId=Q13557-1; Sequence=Displayed;
CC Name=Delta 1;
CC IsoId=Q13557-2; Sequence=Not described;
CC Name=Delta 3;
CC IsoId=Q13557-3; Sequence=Not described;
CC Name=Delta 4;
CC IsoId=Q13557-4; Sequence=Not described;
CC Name=Delta 8;
CC IsoId=Q13557-5; Sequence=Not described;
CC Name=Delta 9;
CC IsoId=Q13557-6; Sequence=Not described;
CC -!- TISSUE SPECIFICITY: EXPRESSED IN CARDIAC MUSCLE AND SKELETAL
CC MUSCLE.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC SUBFAMILY.
CC
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CC
CC EMBL; AF071569; AAD20442.1; --
CC EMBL; AJ252239; CAB65123.1; --
CC EMBL; U50361; AAB16866.1; --
CC HSRF; Q63450; 1A06.
CC Genew; HGNC:1462; CAMK2D.
CC GO; GO:0005524; F:ATP binding activity; NAS.
CC GO; GO:0004685; P:calcium/calmodulin-dependent protein kinase. . .; NAS.
CC GO; GO:0006458; P:protein amino acid phosphorylation; NAS.
CC GO; GO:0001558; P:regulation of cell growth; NAS.
CC InterPro; IPR000719; Prot_kinase.

```

Query Match	Best Local Similarity	Score	DB 1	Length	DB 2	Length	DB 3	Length	DB 4	Length	DB 5	Length	DB 6	Length	DB 7	Length	DB 8	Length	DB 9	Length	DB 10	Length	DB 11	Length	DB 12	Length	DB 13	Length	DB 14	Length	DB 15	Length	DB 16	Length	DB 17	Length	DB 18	Length	DB 19	Length	DB 20	Length	DB 21	Length	DB 22	Length	DB 23	Length	DB 24	Length	DB 25	Length	DB 26	Length	DB 27	Length	DB 28	Length	DB 29	Length	DB 30	Length	DB 31	Length	DB 32	Length	DB 33	Length	DB 34	Length	DB 35	Length	DB 36	Length	DB 37	Length	DB 38	Length	DB 39	Length	DB 40	Length	DB 41	Length	DB 42	Length	DB 43	Length	DB 44	Length	DB 45	Length	DB 46	Length	DB 47	Length	DB 48	Length	DB 49	Length	DB 50	Length	DB 51	Length	DB 52	Length	DB 53	Length	DB 54	Length	DB 55	Length	DB 56	Length	DB 57	Length	DB 58	Length	DB 59	Length	DB 60	Length	DB 61	Length	DB 62	Length	DB 63	Length	DB 64	Length	DB 65	Length	DB 66	Length	DB 67	Length	DB 68	Length	DB 69	Length	DB 70	Length	DB 71	Length	DB 72	Length	DB 73	Length	DB 74	Length	DB 75	Length	DB 76	Length	DB 77	Length	DB 78	Length	DB 79	Length	DB 80	Length	DB 81	Length	DB 82	Length	DB 83	Length	DB 84	Length	DB 85	Length	DB 86	Length	DB 87	Length	DB 88	Length	DB 89	Length	DB 90	Length	DB 91	Length	DB 92	Length	DB 93	Length	DB 94	Length	DB 95	Length	DB 96	Length	DB 97	Length	DB 98	Length	DB 99	Length	DB 100	Length	DB 101	Length	DB 102	Length	DB 103	Length	DB 104	Length	DB 105	Length	DB 106	Length	DB 107	Length	DB 108	Length	DB 109	Length	DB 110	Length	DB 111	Length	DB 112	Length	DB 113	Length	DB 114	Length	DB 115	Length	DB 116	Length	DB 117	Length	DB 118	Length	DB 119	Length	DB 120	Length	DB 121	Length	DB 122	Length	DB 123	Length	DB 124	Length	DB 125	Length	DB 126	Length	DB 127	Length	DB 128	Length	DB 129	Length	DB 130	Length	DB 131	Length	DB 132	Length	DB 133	Length	DB 134	Length	DB 135	Length	DB 136	Length	DB 137	Length	DB 138	Length	DB 139	Length	DB 140	Length	DB 141	Length	DB 142	Length	DB 143	Length	DB 144	Length	DB 145	Length	DB 146	Length	DB 147	Length	DB 148	Length	DB 149	Length	DB 150	Length	DB 151	Length	DB 152	Length	DB 153	Length	DB 154	Length	DB 155	Length	DB 156	Length	DB 157	Length	DB 158	Length	DB 159	Length	DB 160	Length	DB 161	Length	DB 162	Length	DB 163	Length	DB 164	Length	DB 165	Length	DB 166	Length	DB 167	Length	DB 168	Length	DB 169	Length	DB 170	Length	DB 171	Length	DB 172	Length	DB 173	Length	DB 174	Length	DB 175	Length	DB 176	Length	DB 177	Length	DB 178	Length	DB 179	Length	DB 180	Length	DB 181	Length	DB 182	Length	DB 183	Length	DB 184	Length	DB 185	Length	DB 186	Length	DB 187	Length	DB 188	Length	DB 189	Length	DB 190	Length	DB 191	Length	DB 192	Length	DB 193	Length	DB 194	Length	DB 195	Length	DB 196	Length	DB 197	Length	DB 198	Length	DB 199	Length	DB 200	Length	DB 201	Length	DB 202	Length	DB 203	Length	DB 204	Length	DB 205	Length	DB 206	Length	DB 207	Length	DB 208	Length	DB 209	Length	DB 210	Length	DB 211	Length	DB 212	Length	DB 213	Length	DB 214	Length	DB 215	Length	DB 216	Length	DB 217	Length	DB 218	Length	DB 219	Length	DB 220	Length	DB 221	Length	DB 222	Length	DB 223	Length	DB 224	Length	DB 225	Length	DB 226	Length	DB 227	Length	DB 228	Length	DB 229	Length	DB 230	Length	DB 231	Length	DB 232
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	Query Match	22.7%; Score 589.5; DB 1;	Length 374;
	Best Local Similarity	41.6%; Pred. No. 3.6e-23;	
	Matches 124;	Conservative 56;	Mismatches 113; Indels 5; Gaps 4
Qy	18	QTPLRLRDYLLGKKGOGQFCTTTLCTEKSTSANVACKSIPIKRKLVCREDYEDVMREIQI	77
Dd	12	QAEDIRDIYDFRDLVTGTATSEVLAEDRTQKLVAIKCIAKALEGREG--SMNEETAV	69
Qy	78	MHHLSEHPNVVRINKGTYESDSVFVHVMEVCBGGELFDRIIVSGHPFSERAEVKLIKTILGV	137
Dd	70	LHKI-KHPNIVALDDIYESGGHLYLIMQLVSGGELFDRIIVEKGFYTEADASRLIFQVLDA	128
Qy	138	VEACHSLGVMHRRDLKPENFLFDSPKDAAKLKATDPGLSVFYKPGQYLVDWVGSPYYVAPE	197
Dd	129	VKYLDLUGIVHRDLKPENLLYYLUDEDSKIMISDFGSKMEDPQSULSTACGTGCVVAPE	188

PT	MUTAGEN	49		K->A: LOSS OF ACTIVITY.
SQ	SEQUENCE	370 AA;	41337 MW;	57FA20BCE00FA76C CRC64;
	Query Match	22.7%;	Score 587.5;	DB 1; Length 370;
	Best Local Similarity	41.6%;	Pred.No. 4.5e-23;	
	Matches 124;	Conservative 55;	Mismatches 114;	Indels 5; Gaps 4;
Qy	18 QTPRLRDHYLLGKKLGGQGFTGYLTCTEKSTKSANYACKSIPKPKLVCREDDYDVWREIQI	77		
Dd	12 QAEDIRDIYDFRDLVGTGAFFSEVILAEADKRTOKLVAIKCIAKEALGKEG--SMENEIAV	69		
Qy	78 MHHLSEHNPVRIGKTYEDSVFHIIVMEVCEGGEFLDRIVSKGFSERAVKLIKTLGV	137		
Dd	70 LHKI-KHPNIVALDDIYESGGHLYLMQLVSGSELFDRIVEKGFYTERDASRLIFQVLDA	128		
Qy	138 VEACHSLGMVHRDLKPENFLFSDPKDDAKLKATDFGLSVFYKPGQVLYDWVGSPYYVAPE	197		
Dd	129 VKYLHDGLGIHVHRDLKPENLLYYSLDEDSKIMISDFGLSKMEDPFGSVLSTACGTGTVVAPE	188		
Qy	198 VL-KKYCGPEIDVWSAGVITYILLSCVPFPWAETESIGFIQILQGLDKPKSPDPWPITISA	256		
Dd	189 VLAQKPYSKAVDCWSGTGVAYILLCGYPFPYDENADKLFEQILKAIEYEFDSPYWDIDS	248		
Qy	257 AKDLIYKMLERSPKKRISAHEALCHPWIDEQAAPDKPLDPAVLSRLKQFSQWNKTKK	314		
Dd	249 AKDFIRHLMKEKDPEKFTCEALQHFWIAGDTAL-DKNTHQSVSQEIOKKNFAKSWKWQ	305		
 RESULT 13				
ID	KCC4 HUMAN	STANDARD;	PRT;	473 AA.
ID	Q165Z6;			
DC	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DE	15-SBP-2003 (Rel. 42, Last annotation update)			
DE	Calcium/calmodulin-dependent protein kinase type IV catalytic chain			
DN	(BC 2.7.1.123) (CAM Kinase-GR) (CAMK IV).			
GN	CAMK4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
NCBI_TaxID=9606;	[1]			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=94375404; PubMed=8089075;			
RX	Kitani T., Okuno S., Fujisawa H.;			
RA	"CDNA cloning and expression of human calmodulin-dependent protein			
RT	kinase IV.";			
RT	J. Biochem. 115:637-640(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Cerebellum, and Thymus;			
RC	MEDLINE=94252566; PubMed=8194751;			
RX	Bland M.M., Monroe R.S., Ohmsted C.A.;			
RA	"The cDNA sequence and characterization of the			
RT	Ca2+/calmodulin-dependent protein kinase-Gr from human brain and			
RT	thymus";			
RL	Gene 142:191-197(1994).			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Blood;			
RC	MEDLINE=94149862; PubMed=8107230;			
RX	Moskalov G., Hanissian S.H., Jawaahar S., Vara L., Kieff E.,			
RA	Chatila T.A.;			
RA	"A Ca2+/calmodulin-dependent protein kinase, Cam kinase-Gr, expressed			
RT	after transformation of primary human B lymphocytes by Epstein-Barr			
RT	virus (EBV) is induced by the EBV oncogene LMPI."			
RL	J. Virol. 68:1697-1705(1994).			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RP	TISSUE=Brain;			
RC	MEDLINE=22388257; PubMed=12477932;			
RX				

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Rittersch S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smillius D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences".  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- FUNCTION: CALSPERMIN IS A HEAT-STABLE, ACIDIC, CALMODULIN-BINDING  
 CC PROTEIN.  
 CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.  
 CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL  
 CC NUCLEI (BY SIMILARITY).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=2;  
 CC Name=1;  
 CC IsoId=Q16566-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Calpermin;  
 CC IsoId=Q16566-2; Sequence=Not described;  
 CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK  
 CC SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: D30742; BAA06403.1; -  
 CC EMBL: L17000; AAA35639.1; -  
 CC EMBL: L24959; AAA18251.1; -  
 CC EMBL: BC016695; AAH16695.1; -  
 CC PIR: A53036; A53036.  
 CC HSP: Q63450; 1A06.  
 CC Genew: HGNC:1464; CAMK4.  
 CC MIM: 114080; -  
 CC GO: GO:0004685; F:calcium/calmodulin-dependent protein kinase. . .; TAS.  
 CC GO: GO:0004688; P:protein amino acid phosphorylation; TAS.  
 CC GO: GO:0007165; P:signal transduction; TAS.  
 CC InterPro: IPR000719; Prot kinase.  
 CC InterPro: IPR002290; Ser Thr kinase.  
 CC Pfam: PF00069; pkinase; 1.  
 CC ProDom: PD000001; Prot kinase; 1.  
 CC SMART: SM00220; S\_TKc; 1.  
 CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 CC PROSITE: PS00108; PROTEIN KINASE ST; 1.  
 CC PROSITE: PS50011; PROTEIN KINASE DOM; 1.  
 CC Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW Calmodulin-binding; Alternative splicing  
 FT DOMAIN 46 300 PROTEIN KINASE.  
 FT NP\_BIND 52 60 ATP (BY SIMILARITY).  
 FT BINDING 75 75 ATP (BY SIMILARITY).  
 FT ACT\_SITE 164 164 BY SIMILARITY.  
 FT DOMAIN 322 341 CALMODULIN-BINDING (POTENTIAL).  
 SQ SEQUENCE 473 AA; 51925 MW; EFEE51E5612326DC CRC64;  
 Query Match 22.3%; Score 578.5; DB 1; Length 473;  
 Best Local Similarity 37.2%; Pred. No. 1.6e-22;  
 Matches 140; Conservative 65; Mismatches 144; Indels 27; Gaps 10;

QY 22 LRHYLLGKLGQGGTTLCTEKSTSYACKSIPKRLKVCREDYEDVWREIQIMHHL 81  
 DB 42 LSDFFEVESELGRGATSIYVRCKQKGTQKPYALKVLKK-----TVDKKIVRTIGVLLRL 96  
 QY 82 SEHPNVVRIGYVEDSVFHHVMEVCEGEGELPDRIIVSKGHFSREAVKLITKILGVVEAC 141  
 DB 97 S-HPNIIKLEKEIETPTETISLVLVLTGGELEFDRIVEKGYISERDAADAVKQILEAVYL 155  
 QY 142 HSLGVNHRDLKPFENLFDSPKODAKLKATDFGLSVFYKPGQYLYDVVGVPPYVAVPEVLKK 201  
 DB 156 HENGIVHRDLKENLKYATPADAPLKIADFLGSKIVEHQVLMKTVCGTPGYPGCAPEILRG 215  
 QY 202 C-YGPEIDVMSAGVILYILLGVPPFPAET-ESGIFRQILQGLDFKSPWPITISEAAKD 259  
 DB 216 CAYGPEVDMSVGIITILLGFEFPYDGRGQDFMRRLNCEYFISPMWDEVSLNAKD 275  
 QY 260 LYVKMLERSPKRISAEALCHPWIVDEQAADPLDPAVLRLKQFOSOMNKIKKMLRLV 319  
 DB 276 LVKRLIVLDPKRLTTFQALQHPWVTG-KAANFVHMDTA-QKKLOEFNARRKLKAAVYKAV 333  
 QY 320 IA-ERL--SEEEIGGLKELFKM-----IDTNSGTTTFEE-----LKAGLKRGVSE 362  
 DB 334 VASSRLGSSASSHSGSIQESHKASRDPSPIDQGNEDMKAIPEGEKIQGDGAQAQAAVKAQAE 393  
 QY 363 LMSEIKSLMDAADID 378  
 DB 394 LMKVQALEKVGADIN 409  
 RESULT 14  
 KCCD RAT  
 ID KCCD RAT STANDARD; PRT; 533 AA.  
 AC P15791;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Calcium/calmodulin-dependent protein kinase type II delta chain  
 DE (EC 2.7.1.123) (CaM-kinase II delta chain) (CaM kinase II delta  
 DE subunit) (CaMK-II delta subunit).  
 GN CAMK2D.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90036861; PubMed=2553697;  
 RA Tobimatsu T., Fujisawa H.;  
 RT "Tissue-specific expression of four types of rat calmodulin-dependent  
 RL protein kinase II mRNAs";  
 RL J. Biol. Chem. 264:17907-17912(1989).  
 RN [2]  
 RP SEQUENCE OF 314-533 FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Aorta, and Skeletal muscle;  
 RX MEDLINE=93300844; PubMed=8390994;  
 RA Schworer C.M., Rothblum L.I., Thekkumkara T.J., Singer H.A.;  
 RT "Identification of novel isoforms of the delta subunit of  
 RT Ca2+/calmodulin-dependent protein kinase II. Differential expression  
 RT in rat brain and aorta";  
 RL J. Biol. Chem. 268:14443-14449(1993).  
 CC -!- FUNCTION: THIS KINASE MAY PLAY A ROLE IN NEUROTRANSMISSION.  
 CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.  
 CC -!- ENZYME REGULATION: AUTOPHOSPHORYLATION OF CAM-KINASE II PLAYS AN  
 CC IMPORTANT ROLE IN THE REGULATION OF THE KINASE ACTIVITY.  
 CC -!- SUBUNIT: COMPOSED OF FOUR DIFFERENT CHAINS: ALPHA, BETA, GAMMA,  
 CC AND DELTA.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event-Alternative splicing; Named isoforms=4;  
 CC Name=Delta 1;  
 CC IsoId=PI5791-1; Sequence=Displayed;  
 CC Name=Delta 2;  
 CC IsoId=PI5791-2; Sequence=VSP\_004784;  
 CC Name=Delta 3;



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CC      IsoId=p15791-3; Sequence=VSP_004785, VSP_004786, VSP_004787;
CC      Name=Delta 4;
CC      IsoId=p15791-4; Sequence=VSP_004788;
CC      -!- TISSUE SPECIFICITY: DELTA 1 IS THE PREDOMINANT FORM IN THE BRAIN,
CC      DELTA 2 AND 3 PREDOMINATE IN THE AORTA AND DELTA 4 IN SKELETAL
CC      MUSCLE.
CC      -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. CAMK
CC      SUBFAMILY.
CC      -----
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CC      EMBL; J05072; AAA00866.1; -
CC      EMBL; L13406; AAA41479.1; -
CC      EMBL; L13407; AAA41480.1; -
CC      EMBL; L13408; AAA41481.1; -
CC      PIR; A34366; A34366.
CC      HSP; O63450; 1A06.
CC      InterPro; IPR000719; Prot_kinase.
CC      InterPro; IPR002290; Ser_thr_pkinase.
CC      Pfam; PF00069; pkinase; 1.
CC      ProDom; PD000001; Prot_kinase; 1.
CC      SMART; SM0220; S_TKc; 1.
CC      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC      PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC      Transferase; Serine/threonine-protein kinase; Calmodulin-binding;
CC      phosphorylation; ATP-binding; Neurone; Alternative splicing.
CC      DOMAIN 14 272 PROTEIN_KINASE.
CC      NP_BIND 20 28 ATP (BY SIMILARITY).
CC      BINDING 43 43 ATP (BY SIMILARITY).
CC      ACT_SITE 136 136 BY SIMILARITY.
CC      DOMAIN 291 301 Missing (in isoform Delta 2).
CC      VARSPPLIC 329 362 /FTid=VSP_004784.
CC      VARSPPLIC 329 335 INKANV -> KRKSSV (in isoform Delta 3).
CC      VARSPPLIC 337 359 Missing (in isoform Delta 3).
CC      VARSPPLIC 360 362 GNK -> QMM (in isoform Delta 3).
CC      VARSPPLIC 349 362 Missing (in isoform Delta 4).
CC      SEQUENCE 533 AA; 60080 MW; E41BCB2B5A00E7CA CRC64;
CC
CC      Query Match 22.2%; Score 574.5; DB 1; Length 533;
CC      Best Local Similarity 39.4%; Pred. No. 3e-22;
CC      Matches 127; Conservative 54; Mismatches 134; Indels 7; Gaps 5;
CC
CC      QY 21 RLRDHLLGKLGQGGTGYLTCTEKSTANYACKSPKRLVCREDYEDVWRQIMMH 80
CC      Db 9 RFTDEYQLFELGKGFVSVRCMKIPTGQYAAKIINTKLSAR-DHOKLREARIC-R 66
CC
CC      QY 81 LSEHPNVRIKGYEDSVFVHVMEVCEGELFDRIVSKGHFSEAEAVKLITLGVEA 140
CC      Db 67 LLKHPNIVRLHDSISEGFFHYLFDLVGTGELFEDIVAREYSEADASHCIQQLSEVNH 126
CC      QY 141 CHSLGWHRDLKPFNFDFSPKDDAKLKTDFGLSVFYKPGQYL-YDVVGSPYYVAPEVL 199
CC      Db 127 CHLNGIVHRDLKPFNLLASKSGAAVKLADFLGATEVQDQQAQWFGAGTGYLSPEVL 186
CC      QY 200 KK-CYGEIDVWSAGVLYTLTLLSGVPPFAETESGIFRQILQKLPKSPDPTISEAK 258
CC      Db 187 RKDPYKGVDMWACGVLYTLVGYPPFDEQHRLYQQIKAGAYDFPSPEDTDTVTPK 246
CC      QY 259 DLTYKMLERSPKKRIISAHEALCHPWIIVDEQAQPKLDPVLRSLKQFSQMNKIKKMLR 318
CC      Db 247 DLINKMLTINPAKRITASEALKHPVICQRTVSMHRRQETVCLCKFNARRKLKG---A 303
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QY 319 VIAERLSEEEIGGLKELFKMID 340
Db 304 ILTMTLATRNFSAAKSLKKPD 325

RESULT 15
KCC4_MOUSE
ID KCC4_MOUSE STANDARD; PRT; 469 AA.
AC P08414; Q61381;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type IV catalytic chain
DE (EC 2.7.1.123) (CAM kinase-GR) (CaMK IV).
DE CAMK4.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=91372388; PubMed=1893997;
RA Jones D.A., Giod J., Wilson-Shaw D., Hahn W.E., Sikela J.M.;
RT "cDNA sequence and differential expression of the mouse
RT Ca2+/calmodulin-dependent protein kinase IV gene.";
RL FEBS Lett. 289:105-109(1991).
RN [2]
RP SEQUENCE OF 240-469 FROM N.A.
RX MEDLINE=89122027; PubMed=2536634;
RA Sikela J.M., Law M.L., Kao F.-T., Haritz J.A., Wei Q., Hahn W.E.;
RT "Chromosomal localization of the human gene for brain
RT Ca2+/calmodulin-dependent protein kinase type IV.";
RL Genomics 4:21-27(1989).
RN [3]
RP SEQUENCE OF 315-469 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87204263; PubMed=3033675;
RA Sikela J.M., Hahn W.E.;
RT "Screening an expression library with a ligand probe: isolation and
RT sequence of a cDNA corresponding to a brain calmodulin-binding
RT protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:3038-3042(1987).
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- SUBCELLULAR LOCATION: SUBSTANTIAL LOCALIZATION IN CERTAIN NEURONAL
CC NUCLEI.
CC -!- TISSUE SPECIFICITY: BRAIN AND TESTIS.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC CAMK SUBFAMILY.
CC -----
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CC EMBL; M16206; AAA39933.1; -
CC EMBL; M4266; AAA37364.1; -
CC EMBL; J03057; AAA37366.1; -
CC EMBL; X58995; CAA41741.1; -
CC PIR; S17656; S17656.
CC HSP; Q63450; 1A06.
CC MGD; MG1:88258; Camk4.
CC GO; GO:0016563; F:transcriptional activator activity; IMP.
CC GO; GO:0007270; P:nervous system synaptic transmission; IMP.
CC GO; GO:0006468; P:protein amino acid phosphorylation; IMP.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 1.
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DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00108; PROTEIN KINASE ST; 1.
DR PROSITE; PS00111; PROTEIN KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Calmodulin-binding.
FT DOMAIN 42 296 PROTEIN KINASE.
FT NP_BIND 48 56 ATP (BY SIMILARITY).
FT BINDING 71 71 ATP (BY SIMILARITY).
FT ACT_SITE 160 160 BY SIMILARITY.
FT DOMAIN 318 337 CALMODULIN-BINDING (POTENTIAL).
FT CONFLICT 278 280 VLD -> CFGI (IN REF. 2).
FT CONFLICT 302 302 N -> T (IN REF. 2).
SQ SEQUENCE 469 AA; 52627 MW; CE1F986708222F975 CRC64;

Query Match 22.1%; Score 574; DB 1; Length 469;
Best Local Similarity 33.4%; Pred. No. 2.7e-22;
Matches 146; Conservative 79; Mismatches 170; Indels 42; Gaps 12;

QY 22 LRDHYLLGKLGQGGFTYLLCTEKSTANSYACKSIPKRKLVCREYEDVWREIQIMHHL 81
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
38 LGDFEVESELGRGATSIYVRCKQKGTQKPYALKVLK-----TVDKKIVRTEIGVLLRL 92
QY 82 SHPNVVR1KGYEDSVFVHIVMEVCEGGELEDRIVSKGHFSERAVKLIKILGVVEAC 141
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
93 S-HPNIIKLKEIFETPTSEISLVLELVTGGELFDRIVEKGYSERDARDAVKQILEAVAYL 151
QY 142 HSLGVMHRLDKPENLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVGSPPYVAPEVLKK 201
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
152 HENGIVHRDLKENLLYATPADAPLKIADFGLSKIVEHQVLMKTVCGTFGYCAPEILRG 211
QY 202 C-YGPEIDVWSAGVILYILLSGVPPFWAET-ESGIFRQILQKGLDFKSDPWPTI SEAAKD 259
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
212 CAYGPEVDMWSVGIITYILLCGFEPFYDERGQFMFRILNCEYYFISPWDEVSINAKD 271
QY 260 LIYKMLERSPKKRI SAHEALCHPWIVDEQAAAPDKPLDPAVL SRLKQFSOMNKIKKALRV 319
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
272 LVKKLIVLDPKKRLTTFQALQHPWVG-KAANFVHMDTA-QKKLOEFNARRKKAQAVKAV 329
QY 320 IAERLSEEEIGGLKELFKMIDTD---NSGTITFEELKAGLKRVGSELMESEIKSLMDAAD 376
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
330 VA-----SSRLGSASSSHTSIQENHKASSDPPSTQDAKOSTDLLGKKMQEEDQEE----- 379
QY 377 IDNSTIDYGEPLAATLHNKMERBEILVAAFSDFDKGSGYITIDELQSACTEFGLCDT 436
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
380 -----DQVEAEASADEMRKLQSEV-----EKDAG--VKEEETSSMVPQDPEDEL 422
QY 437 PLDDMIKEIDLNDGKI 453
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
423 ETDD--PENKRDSEKL 437
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Search completed: November 28, 2003, 10:32:03  
Job time : 26 secs

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OM protein - protein search, using sw model

Run on: November 28, 2003, 10:31:21 ; Search time 26 Seconds

(without alignments)  
805.534 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRRPSNTVLPQPTP.....KNLNFNIADAFGVGKSD 495

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Parents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1927	74.3	463	1 US-07-951-715A-25	Sequence 25, Appl
2	1927	74.3	463	2 US-08-459-448A-25	Sequence 25, Appl
3	1927	74.3	463	3 US-08-459-595A-25	Sequence 25, Appl
4	1927	74.3	463	3 US-08-459-504B-25	Sequence 25, Appl
5	1927	74.3	463	3 US-08-459-444-25	Sequence 0, Appli
6	1927	74.3	463	3 US-09-547-422-25	Sequence 0, Appli
7	1672.5	64.5	639	3 US-09-347-801-17	Sequence 17, Appl
8	1437.5	55.4	464	1 US-07-951-715A-22	Sequence 22, Appl
9	1437.5	55.4	464	2 US-08-459-448A-22	Sequence 22, Appl
10	1437.5	55.4	464	3 US-08-459-595A-22	Sequence 22, Appl
11	1437.5	55.4	464	3 US-08-459-504B-22	Sequence 22, Appl
12	1437.5	55.4	464	3 US-08-459-444-22	Sequence 0, Appli
13	1437.5	55.4	464	4 US-09-547-422-22	Sequence 0, Appli
14	1277.5	49.3	408	1 US-07-951-715A-21	Sequence 21, Appl
15	1277.5	49.3	408	2 US-08-459-448A-21	Sequence 21, Appl
16	1277.5	49.3	408	3 US-08-459-595A-21	Sequence 21, Appl
17	1277.5	49.3	408	3 US-08-459-504B-21	Sequence 21, Appl
18	1277.5	49.3	408	3 US-08-459-444-21	Sequence 21, Appl
19	1277.5	49.3	408	4 US-09-547-422-21	Sequence 21, Appl
20	829	32.0	623	3 US-09-347-801-4	Sequence 4, Appli
21	826	31.9	625	3 US-09-347-801-18	Sequence 4, Appli
22	800	30.3	576	3 US-09-347-801-19	Sequence 18, Appl
23	771.5	29.8	456	1 US-08-464-164-2	Sequence 2, Appli
24	771.5	29.8	456	1 US-08-338-057-2	Sequence 2, Appli
25	771.5	29.8	456	2 US-08-668-416-2	Sequence 2, Appli
26	622	24.0	520	4 US-09-257-825B-20	Sequence 20, Appl
27	587.5	22.7	370	2 US-08-878-989-19	Sequence 19, Appl

Sequence 19, Appl  
Sequence 31, Appl  
Sequence 21, Appl  
Sequence 10, Appl  
Sequence 19, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 18, Appl  
Sequence 1, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 30, Appl  
Sequence 5, Appl  
Sequence 5, Appl  
Sequence 23, Appl  
Sequence 23, Appl

#### ALIGNMENTS

##### RESULT 1

US-07-951-715A-25

; Sequence 25, Application US/07951715A

; Patent No. 5625136

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-GEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30B

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/07/951,715A

; FILING DATE: 25-SEP-1992

; CLASSIFICATION: 800

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/772,027

; FILING DATE: 04-OCT-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Spruill, W. Murray

; REGISTRATION NUMBER: 32,943

; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (919)541-8615

; TELEFAX: (919)541-8689

```

; INFORMATION FOR SEQ ID NO: 25:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 463 amino acids
;     TYPE: amino acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: protein
;     HYPOTHETICAL: NO
;     FEATURE:
;         NAME/KEY: Protein
;         LOCATION: 1..463
;         OTHER INFORMATION: /note=
;
; US-07-951-715A-25
;
; OTHER INFORMATION: soybean

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Query Match	74.3%	Score 1927;	DB 1;	Length 463;
Best Local Similarity	78.7%;	Pred. No. 1.3e-152;		
Matches	365;	Conservative 49;	Mismatches 48;	Indels 2; Gaps 2; 1;
QY	14	VLPYQTPRLRDHYLLGKKLQGOFGTGYLTCTEKSTANYACKSIPKRLKVCREDYEDVWR	73	
DB	1	VLPQRTQNIREVYEVGRKLQGOFGTTFCTRASGGKFACKSIPKRLKLUCKEDYEDVWR	60	
QY	74	ETQIMHHLSEHPNVVRIKGTYESVSFVHIIVMEVCEGELFDRIVSGKHGFSEAVKLIKT	133	
DB	61	ETQIMHHLSEHANVVRIGETYESDVAHLVMEICEGELFDRIVQKHYSERQAARLIKT	120	
QY	134	IIVGVAEACHSLGVMMHRDLKPNELFDPSPKDDAKLKATDFGLSVFYKPGOYLYDVWGSPYY	193	
DB	121	IIVGVAEACHSLGVMMHRDLKPNELFDTIDEDAKLKATDFGLSVFYKPGESFCDVWGSPYY	180	
QY	194	VAPEVLKKCYGPBIDVWSAGVILIYLLSGVPPFWAETESGIFRQIILQGLDKFSKDPWPTI	253	
DB	181	VAPEVLKLYGPESDVWSAGVILIYLLSGVPPFWAERSEPGIFRQIILGLKDFHSEWPSSI	240	
QY	254	SBAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQWNKIK	313	
DB	241	SDSAKDLIRKMLDQNPKEKRLTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSANWKLK	300	
QY	314	KNALRVIAERLSEEEIGGKLFKPMIDTQNSGTTTFEELKAGLRKRVGSELMSEIKSLMD	373	
DB	301	KNALRVIAERLSEEEIGGKLFKPMIDTQNSGTTTFDELKQGLKRVGSELMSEIKSLMD	360	
QY	374	AADIDNSGTTIDYGEFLAATLHNKMKEREELVAAFSDFKDQSGYITIDELQACTFERGL	433	
DB	361	AADIDKSGTIDYGEFLAATVHLNKLREENLVAFSYFDKQSGYITIDELIQOACKDFGL	420	
QY	434	CDTPDDMMIKETDLNDGKIDSEFTMMRMKGD-VGVRSRRTMMK	476	
DB	421	DDIHDMMIKETDQNDGQIDYGEFAAMRMKNGGIGIR-RTWRK	463	

RESULT 2  
US-08-459-448A-25  
Sequence 25, Application US/08459448A  
Patent No. 5859336  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalin M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.

```

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 5859336artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; STREET: Rd., POB 2005
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,448A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8582
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 463 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..463
; OTHER INFORMATION: /note= "protein sequence for
; OTHER INFORMATION: soybean CDPK as shown in Figure 34."
US-08-459-448A-25

```

Query Match	74.3%;	Score 1927;	DB 2;	Length 463;
Best Local Similarity	78.7%;	Pred. No. 1.3e-152;		
Matches	365;	Conservative 49;	Mismatches 48;	Indels 2; Gaps 2;
QY	14	VLPIQTPRLRDHYLLGKKLGGQGFQGTYYLCTEKSTSAN YACKSIPIRKLVCREDYEDVWR	73	
DB	1	VLPIQTONIREYVEVRKLGQGFQGTTFCTRASRGKFAKSIPIRKLCLKEDYEDVWR	60	
QY	74	EQIMHLSSEHPNVRIKGTYESDVFVHVIMEVCEGGEFLDRTVSKGHSESAVKLIKT	133	
DB	61	EQIMHLSSEHANVRIEGTYESDSTAVHLVMEUCEGGEFLDRIQVKGHSYERAAKLIKT	120	
QY	134	IIGVVEACHSLGVMHRDLKPENFLFDPSPKDDAKLKATDFGLSVFYKPGQYLVDVWGSPYY	193	
DB	121	IVEVVEACHSLGVMHRDLKPENFLFDTIDEDAKLKATDFGLSVFYKPGSEFCDVWGSPYY	180	
QY	194	VAPEVLKCYGPEIDVWSAGVITYLLSGVPPFPFAETESGIFRQILQGLKDPKSDPWPT	253	
DB	181	VAPEVRLKLYGPESDVWSAGVITYLLSGVPPFPFAESEPGIFRQILLGLKDFHSEWPSSI	240	
QY	254	SEAAKDLIVKMLERSEPKKRI SAHEALCHPWIVDEQAAAPDKLPDPAVLSRLKQFSOMNKTK	313	
DB	241	SDSAKDLTRKMLDQNPKTRLTAEVLRHPWIVDDNIAPDKLPDSAVLSRLKQFSAMNKUK	300	
QY	314	KWALRVIAERLSEEEIGGLKELFKMIDTNSGTITIFELKAGLKRVGSELMSEIKSLMD	373	

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Db 301 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTDELKDLGLKRVGSELMSESEIKDLM 360
QY 374 AADINSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFL 433
Db 361 AADIDKSGTIDYGEFLAATVHLNKLREENLVSAFSDYFDKDGSGYITLDEIOQACKDFGL 420
QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476
Db 421 DDIIHDDMIKEIDQNDGQIDYGEFAAMRMKNGNGGIGR-RTMRK 463
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## RESULT 3

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US-08-459-595A-25
; Sequence 25, Application US/08459595A
; Patent No. 6018104
```

## GENERAL INFORMATION:

```
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, John L.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
```

```
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
```

## NUMBER OF SEQUENCES: 94

## CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: No. 6018104artis Corporation
; STREET: Patent & Trademark Dept., 520 White Plains
; CITY: Tarrytown
; STATE: New York
; COUNTRY: USA
; ZIP: 10591-9005
```

## COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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## CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/459.595A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Pace, Gary M.
; REGISTRATION NUMBER: 40403
```

## REFERENCE/DOCKET NUMBER: C0C 1577/CIP/DIV3

## TELECOMMUNICATION INFORMATION:

```
; TELEPHONE: (919)541-8582
```

```
; TELEFAX: (919)541-8689
```

## INFORMATION FOR SEQ ID NO: 25:

## SEQUENCE CHARACTERISTICS:

```
; LENGTH: 463 amino acids
```

```
; TYPE: amino acid
```

```
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
```

```
; MOLECULE TYPE: protein
```

```
; 
```

```
; 
```

```
; 
```

```
; 
```

```
; 
```

```
; 
```

```
; 
```

## HYPOTHETICAL: NO

## FEATURE:

```
; NAME/KEY: Protein
```

```
; LOCATION: 1..463
```

```
; OTHER INFORMATION: /note= "protein sequence for
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```
; OTHER INFORMATION: soybean CDPK as shown in Figure 34."
```

```
US-08-459-595A-25
```

## Query Match

```
Best Local Similarity 74.3%; Score 1927; DB 3; Length 463;
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Mismatches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;
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QY 14 VLPYQTPLRLRDHYLLGKKGQGFQTTLYLCTKTSANVACKSIIPKRLVKREDYEDVNR 73
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Db 1 VLPQRTQNIREVYEVGRKLGQGFQTTTCTRAGGRKACKSIIPKRLVKREDYEDVNR 60
```

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QY 74 EIQIMHILSEHPNVVRIRKGTDEDSVFVHIVMVEVCEGELFDRIVKSGHFSEAEVKLIKT 133
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```
Db 61 EIQIMHILSEHANVVRIEGTYEDSTAVHLVMEICEGELFDRIVQKGHYSERQAARLIKT 120
```

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QY 134 ILGVVEACHSLGVMEHDLKPNFLFDSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193
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```
Db 121 IVEVVEACHSLGVMEHDLKPNFLFDTTIDEDAKLKATDFGLSVFYKPGESFCDVVGSPY 180
```

```
QY 194 VAPEVLKKCYGPEIDVWSAGVILYILLSGVPPFMAETESGIFRQILQGLDFKSDPWPPTI 253
```

```
Db 181 VAPEVLKLYGPESDVNSAGVILYILLSGVPPFMAESEPGIFRQILGLKDFHSEPPPSI 240
```

```
QY 254 SEAAKDLIYKMLERSPKKRIISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSOMNKIK 313
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Db 241 SDSAKDLIRKMLDQNPKTRLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300
```

```
QY 314 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTDEELKAGLKRVSSELMSESEIKSLMD 373
```

```
Db 301 KVALRVIAERLSEEEIGGLKELFKMIDTNSGTTTDELDKGLKRVGSELMSESEIKDLM 360
```

```
QY 374 AADINSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFL 433
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Db 361 AADIDKSGTIDYGEFLAATVHLNKLREENLVSAFSDYFDKDGSGYITLDEIOQACKDFGL 420
```

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QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476
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Db 421 DDIIHDDMIKEIDQNDGQIDYGEFAAMRMKNGNGGIGR-RTMRK 463
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## RESULT 4

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US-08-459-504B-25
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; Sequence 25, Application US/08459504B
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; Patent No. 6075185
```

## GENERAL INFORMATION:

```
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
```

## NUMBER OF SEQUENCES: 94

## CORRESPONDENCE ADDRESS:

```
; ADDRESSEE: No. 6075185artis Corporation
```

```
; STREET: 3054 Cornwallis Road
```

```
; CITY: Research Triangle Park
```

STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..463  
OTHER INFORMATION: /note= "protein sequence for  
soybean CDPK as shown in Figure 34."  
US-08-459-504B-25

Query Match 74.3%; Score 1927; DB 3; Length 463;  
Best Local Similarity 78.7%; Pred. No. 1.3e-152;  
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPTQPLRDLHYLLGKLGQGGFTYLTCTEKSTSANVACKSIIPKRLVCREDYEDVWR 73  
Db 1 VLPTQPLRDLHYLLGKLGQGGFTYLTCTEKSTSANVACKSIIPKRLVCREDYEDVWR 60  
QY 74 EIQIMHLLSEHPNVRIKGTYESVVFHVMVECEGELFDRIVSKGHFSREAVKLKT 133  
Db 61 EIQIMHLLSEHPNVRIKGTYESVVFHVMVECEGELFDRIVSKGHFSREAVKLKT 120  
QY 134 ILGVVEACHSLGVMHRLDLPENFLFDSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYY 193  
Db 121 ILGVVEACHSLGVMHRLDLPENFLFDSPKDDAKLKATDGLSVFYKPGQYLDVVGSPYY 180  
QY 194 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 253  
Db 181 VAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQGLKDFKSDPWTI 240  
QY 254 SAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKLPDPAVLRLKQFSQNNKTK 313  
Db 241 SAAKDLIYKMLERSPKKISAEALCHPWIVDEQAAPDKLPDPAVLRLKQFSQNNKTK 300  
QY 314 KVALRVIAERLSEETGGELKFKMTDNTSGTITFEELKAGLKRVSSELSKSLMD 373  
Db 301 KVALRVIAERLSEETGGELKFKMTDNTSGTITFEELKAGLKRVSSELSKSLMD 360  
QY 374 AADINSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFL 433  
Db 361 AADINSGTIDYGEFLAATLHMNMEREELVAAFSDFDKGSGYITIDELQSACTEFL 420

QY 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRSTMMK 476  
Db 421 DDIIHDDMIKEIDLNDGQIDYGEFAAMMRKGGIGR-RTMRK 463  
RESULT 5  
US-08-459-444-25  
Sequence 0, Application US/08459444A  
Patent No. 6121014  
GENERAL INFORMATION:  
APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauris, Karen L.  
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED  
NUCLEIC ACID CODING SEQUENCE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: /note= "protein sequence for  
soybean CDPK as shown in Figure 34."  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..463  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-08-459-444-25

Query Match 74.3%; Score 1927; DB 3; Length 463;  
Best Local Similarity 78.7%; Pred. No. 1.3e-152;  
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;

QY 14 VLPTQPLRDLHYLLGKLGQGGFTYLTCTEKSTSANVACKSIIPKRLVCREDYEDVWR 73  
Db 1 VLPTQPLRDLHYLLGKLGQGGFTYLTCTEKSTSANVACKSIIPKRLVCREDYEDVWR 73

Db 1 VLPQTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRLCKEDYEDVWR 60  
Qy 74 EIQIMHLSHPNVRLKGTVEDSVFVHIVMEVCEGGELEFDRIVSKGHFSREAVKLKT 133  
Db 61 EIQIMHLSHANVVRLEGTYEDSTAVHVMELCEGGELEFDRIVKGYHSEQAARLKT 120  
Qy 134 ILGVVEACHSLGVNHRDLKPNFLFDSPPKODAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
Db 121 IVEVVEACHSLGVNHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGSECDVVGSPPY 180  
Qy 194 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDPKSDPWTI 253  
Db 181 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDPKSDPWTI 240  
Qy 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPAVLSRLKQFSOMNKK 313  
Db 241 SDSAKDLIRKMLDQNPTRLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300  
Qy 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 373  
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 360  
Qy 374 AADIDNSGTTIDYGEFLAATLHMNMKWEREEILVAAFSDFDKDGSYITIDELQSACTEGL 433  
Db 361 AADIDNSGTTIDYGEFLAATLHMNMKWEREEILVAAFSDFDKDGSYITIDELQSACTEGL 420  
Qy 434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476  
Db 421 DDHIDDDMIKEIDQDNDGQIDYGEFAAMMRKGGIGR-RTMRK 463

## RESULT 6

US-09-547-422-25  
; Sequence 0, Application US/09547422  
; Patent No. 6320100  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.  
; Warren, Gregory W.  
; Erola, Stephen V.  
; Crossland, Lydie D.  
; Wright, Martha S.  
; Merlin, Ellis J.  
; Launis, Karen L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: "US/09/547,422  
; FILING DATE: 11-Apr-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/459,595  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:

; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-18805H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: /note= "protein sequence for  
; soybean CDPK as shown in Figure 34."

## SEQUENCE CHARACTERISTICS:

; LENGTH: 463 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO  
; FEATURE:

; NAME/KEY: Protein

; LOCATION: 1..463

; SEQUENCE DESCRIPTION: SEQ ID NO: 25:

US-09-547-422-25

Query Match 74.3%; Score 1927; DB 4; Length 463;  
Best Local Similarity 78.7%; Pred. No. 1.3e-152;  
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;  
Qy 14 VLPQTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRLCKEDYEDVWR 73  
Db 1 VLPQTQNIREVYEVGRKLGQGGQGTTFECTRRASGGKFACKSIPKRLCKEDYEDVWR 60  
Qy 74 EIQIMHLSHPNVRLKGTVEDSVFVHIVMEVCEGGELEFDRIVSKGHFSREAVKLKT 133  
Db 61 EIQIMHLSHANVVRLEGTYEDSTAVHVMELCEGGELEFDRIVKGYHSEQAARLKT 120  
Qy 134 ILGVVEACHSLGVNHRDLKPNFLFDSPPKODAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
Db 121 IVEVVEACHSLGVNHRDLKPNFLFDITDEDAKLKATDFGLSVFYKPGSECDVVGSPPY 180  
Qy 194 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDPKSDPWTI 253  
Db 181 VAPVLKCKYGPEDVMSAGVILYLLSGVPPFWAETESGIFRQILOGKLDPKSDPWTI 240  
Qy 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPAVLSRLKQFSOMNKK 313  
Db 241 SDSAKDLIRKMLDQNPTRLTAEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300  
Qy 314 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 373  
Db 301 KMLRVIAERLSEEEIGGLKELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 360  
Qy 374 AADIDNSGTTIDYGEFLAATLHMNMKWEREEILVAAFSDFDKDGSYITIDELQSACTEGL 433  
Db 361 AADIDNSGTTIDYGEFLAATLHMNMKWEREEILVAAFSDFDKDGSYITIDELQSACTEGL 420  
Qy 434 CDTPLDDMIKEIDLDNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476  
Db 421 DDHIDDDMIKEIDQDNDGQIDYGEFAAMMRKGGIGR-RTMRK 463

## RESULT 7

US-09-347-801-17  
; Sequence 17, Application US/09347801  
; Patent No. 6262345  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/347,801  
; CURRENT FILING DATE: 1999-07-02  
; EARLIER APPLICATION NUMBER: 60/092,438  
; EARLIER FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97

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; SEQ ID NO 17
; LENGTH: 639
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-801-17

Query Match      64.5%; Score 1672.5; DB 3; Length 639;
Best Local Similarity 66.2%; Pred. No. 3.3e-131;
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

QY 5 PNPR-RPS-----NTVLPYQTPRLRDHYLLGKLGQGGTGYLCTEKSYSANY 52
Db 120 PSRPRPOVKRVSSAGLLGSLVLRKNTENLKDYSGLRRLGQGGTGYLCTEKSYSANY 179
QY 53 ACKSPKPKLVCREYEDVWREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGEL 112
Db 180 ACKSLKRLKSGDDVEDVREIQIMHLSHPNVRIKGTVEDSVFVHIVMEVCEGEL 239
QY 113 FDRIVSKGHFSEREAVKLIKITLGVVEACHSGVNMHRLKPNFLFDSPKDDAKLKATDF 172
Db 240 FDRIVRRGHYTERKAAELARVTVGVVEACHSGVNMHRLKPNFLFADHSEEAALKTTDF 299
QY 173 GLSVFYKPGQVLYDVVVGSPYYVAPVVKKCYGPEIDVMSAGVILYILLSGVPPFAETES 232
Db 300 GLSIFFRGQIFTDVVGSPYYVAPVVKKCYGPEIDVMSAGVILYILLSGVPPFAETES 359
QY 233 GIFRQILQGLKDFSDPMTPTISEAAKOLYKMLERSPKKRISAHEALCHPWIVDEQAAPD 292
Db 360 GIFEEVLHGRLDSESEWPSISDGAOLVRLMRYDRPKRLTAHEVLRHPWVQGVAPD 419
QY 293 KLPDPAVLRLKQFSQNMKI KKMALRVIAERLSEEEIGLKLKELFKMIDTDSNGTITFEEL 352
Db 420 RPLDSAVLSRMKQFSQNMKI KKMALRVIAERLSEEEIGLKLKELFKMIDTDSNGTITFEEL 479
QY 353 KAGLKRVGSELMSESEIKSLMDAADDNSGTIDYGEFLAATLHMNMKREELVAAFSDFD 412
Db 480 KVGLEKVGANLQSEIYALMQAADVNNGTIDYGEFIATLHLMNKVEREDHLFAAFQYFD 539
QY 413 KDGSGYITIDELQSACTEFGCLDPLDDMIKEIDLNDNGKIDFSEFTAMMRKGGVGRSR 472
Db 540 KDGSGYITADELQVACEBFGDLGVQLEDLIGEVQDNDGRIDYNEFVAMQK-PTVGSR 598

RESULT 8
US-07-951-715A-22
; Sequence 22, Application US/07951715A
; Patent No. 5625136
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttie, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA

; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 464 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; NAME/KEY: Protein
; LOCATION: 1..464
; OTHER INFORMATION: /note= "derived protein sequence of
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."
US-07-951-715A-22

Query Match      55.4%; Score 1437.5; DB 1; Length 464;
Best Local Similarity 60.9%; Pred. No. 8.4e-112;
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGQGGTGYLCTEKSYSANYACKSIPKRLVCREYEDVWREIQIMHHL 81
Db 9 VRATYSNGKELGRGQGVTHLCTHRTSGEKLACKTIARKLAAREDDVDRREVIQIMHHL 68
QY 82 SEHPNVVRIKGTVEDSVFVHIVMEVCEGELFDRIVSKGHFSEREAVKLIKITLGVVEAC 141
Db 69 SGQPNVVLGRGAYEDKOSVHLVWELCAGGELFDRIIARGQYTERGAELRLAIQIVHTC 128
QY 142 HSLGVNHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPGQVLYDVVVGSPYYVAPVVKK 201
Db 129 HSMGVNHRDLKPNFLFDSKDEDAPLKATDFGLSVFFKEGELLARDIVGSAYYIAPVVKR 188
QY 202 CYGPEIDVMSAGVILYILLSGVPPFAETESGIFRQILQGLKDFPKSDPMTPTISEAAKDLI 261
Db 189 KYGPEADINSGVGMVLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPPWPHISPGAKDLV 248
QY 262 YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQNMKI KKMALRVIA 321
Db 249 KQMLNINPKRLTAFOVLNHPWIKEDGADPTDLNVDRLKQFRANNOFKKALRLIIA 308
QY 322 ERLSEEEIGLKLKELFKMIDTDSNGTITFEELKAGLKRVGSELMSESEIKSLMDAADDNSG 381
Db 309 GCLSEBEITGLKEMFKNIDKNSGTITLDELKHLGAKHPKLSDESEMEKLEAADAAGNG 368
QY 382 TIDYGEFLAATLHMNMKREELVAAFSDFDKGSGYITIDELQSACTEFGCLDPT-PLDD 440
Db 369 LIDYDEFVATVHMNKLDRHEHLYTAFQYDFDKNSGYITKEELEHALKEQGLYDADKID 428
QY 441 MIKEIDLNDNGKIDFSEFTAMMRKG 465
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 9
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US-08-459-448A-22  
; Sequence 22, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, John L.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5859336artis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,448A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40403  
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
; TELEPHONE: (919)541-8582  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 464 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..464  
; OTHER INFORMATION: /note= "derived protein sequence of  
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."  
US-08-459-448A-22  
Query Match 55.4%; Score 1437.5; DB 2; Length 464;  
Best Local Similarity 60.9%; Pred. No. 8.4e-112;  
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;  
22 LRDHVLLGKLGQGGFGTTLCTERSTSNACKSIPKRLVCREDYEDVWREIQIMHHL 81

Db 9 VRATYSMGKELGRGQFGVTHLCTHRTSGEKLACKTKIAKRLAAREDDVDVRRVQIMHHL 68  
QY 82 SEHPNVRRIKGTYESDVFIHVEVCEGGELPDRIVSKGHFSEBAVKLIKTLGVVEAC 141  
Db 69 SGQPNVGLRGAYEDKQSVHLMELCAGGELPDRIIARGQYTERGAELRAIVQIVHTC 128  
QY 142 HSLGVNHRDLKPNFLFDSPKDAKLKATDFGLSVFVKPGQYLYDVVGVSPYYVAPEVLKK 201  
Db 129 HSMGVNHRDIKPNFLLLSKDEDAPLKATDFGLSVFVKEGELLRDVGSAIYIAPVLR 188  
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQIQLOKLDKSPNPTISEAAKDLI 261  
Db 189 KYGPEADIMSVGMVLYIFLAGVPPFWAENENGIFTAILRQQLDLSSEPMPHISPGAKDLV 248  
QY 262 YKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLRLKQFQOMNKKKMAALRVIA 321  
Db 249 KXMLNINPKERLTAFQVLNHPWIKEDGDAPDPTDLNVVLDRLKQFRAMNQFKAALRIIA 308  
QY 322 ERLSEEEIGLKLKELFKMIDTNSGTTTFEELKAGLRVSGSELMSEIKSLMDAADIDNSG 381  
Db 309 GCLSEEEITGLKEMFNKIDKNSGTTITDELKHGLAKHGPKLSDSEWEKMEAADADNG 368  
QY 382 TIDYGEFLAATLHMNMKEREELVAAFSDFDKDGGYITIDELQSACTEFGLCDT-PLDD 440  
Db 369 LIDYDEFVTATVMNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEQGLYDADKID 428  
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465  
Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 10  
US-08-459-595A-22  
; Sequence 22, Application US/08459595A  
; Patent No. 6018104  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6018104artis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,595A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40403  
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
; TELEPHONE: (919)541-8582  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 464 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: Protein  
; LOCATION: 1..464  
; OTHER INFORMATION: /note= "derived protein sequence of  
; OTHER INFORMATION: pollen specific CDPK as disclosed in Figure 34."  
US-08-459-448A-22



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403  
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..464  
OTHER INFORMATION: /note= "derived protein sequence of  
US-08-459-595A-22  
Query Match 55.4%; Score 1437.5; DB 3; Length 464;  
Best Local Similarity 60.9%; Pred. No. 8.4e-112;  
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;  
QY 22 LRHYLLGKLGQGFQGTTLCTEKSSTANYACKSIPKRLVCRDIEDVWREIQIMHHL 81  
DB 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLACKTIAKRLAAREDDVDRREVQIMHHL 68  
QY 82 SEHPNVVRIKGYEDSVFVHIVMEVCEGGELEFDRIVSKGHFSEBAVKLTKILGVVEAC 141  
DB 69 SGQPNVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC 128  
QY 142 HSLGVMRDLKPNFLPDSKDDAKLKATDFGLSVFPGQYLVVGVSPYVAPVLLK 201  
DB 129 HSMGVMRDLKPNFLLSKDDAPLKTATDFGLSVFFKEGELLRDIVGSAYYIAPEVLR 188  
QY 202 CYPEIDVWAGVILYLLSGVPPFWAETSGIFRQILQKGLDFKSPWPTTISEAAKDLI 261  
DB 189 KYGPEADINSGVVMYIFLAGVPPFWAENENGIFTALRGOLDLSSEPPWHISPGAKDLV 248  
QY 262 YKMLERSPKRISAHEALCHPWIVDEQAAPDKPLDPVLSRLKQFSQMNKIKKVALRVIA 321  
DB 249 KKMNLNPKRLTAFQVNLHPWIKEDGDAPDPTPLDNVLDRLKQFRANNOFKKAALRIIA 308  
QY 322 ERLSEEBIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELMSEIKSLMDAADINDSG 381  
DB 309 GCLSEEBITGLKEMFKNDKNSGTITLDELKHLAKHGPKLSDSENEKLEAARDADGNG 368  
QY 382 TIDYGEFLATLHNKMEREILVAAPSDFDKCGSVITIDELQSACTEFLGCDT-PLDD 440  
DB 369 LIDYDEFVATVHMKLDREHLYTAFQYFDKNSGYITKEELEHALKEQGLYDADKID 428  
QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465  
DB 429 IISDADSDNDGRIDYSEFVAMMRKG 453

RESULT 11  
US-08-459-504B-22  
Sequence 22, Application US/08459504B  
Patent No. 6075185  
GENERAL INFORMATION:  
APPLICANT: Kozziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: No. 6075185artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patencin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA: US 08/459,595  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..464  
OTHER INFORMATION: /note= "derived protein sequence of  
US-08-459-504B-22  
Query Match 55.4%; Score 1437.5; DB 3; Length 464;  
Best Local Similarity 60.9%; Pred. No. 8.4e-112;  
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;  
QY 22 LRHYLLGKLGQGFQGTTLCTEKSSTANYACKSIPKRLVCRDIEDVWREIQIMHHL 81  
DB 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLACKTIAKRLAAREDDVDRREVQIMHHL 68  
QY 82 SEHPNVVRIKGYEDSVFVHIVMEVCEGGELEFDRIVSKGHFSEBAVKLTKILGVVEAC 141  
DB 69 SGQPNVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC 128

Query Match 55.4%; Score 1437.5; DB 3; Length 464;  
Best Local Similarity 60.9%; Pred. No. 8.4e-112;  
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;  
QY 22 LRHYLLGKLGQGFQGTTLCTEKSSTANYACKSIPKRLVCRDIEDVWREIQIMHHL 81  
DB 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLACKTIAKRLAAREDDVDRREVQIMHHL 68  
QY 82 SEHPNVVRIKGYEDSVFVHIVMEVCEGGELEFDRIVSKGHFSEBAVKLTKILGVVEAC 141  
DB 69 SGQPNVGLRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC 128

142 HSLGVNHRDLKPENFLSPKODAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPVLKK 201  
129 HSGVMVHRDLKPENFLSKDEADPLKATDFGLSVFKEGELLRDIVGSAYYIAPEVLKR 188  
202 CYGPEIDVNSAGVILYLLSGVPPFWAETESGIFROILOGLKLDKDFSDPMTTISEAAKDLI 261  
189 KYGPEADIVSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISPGAKDLV 248  
262 YKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPAVLRSRLKQFSOMNKIKKMLRVIA 321  
249 KQMLNINPKERLTAFQVLNHPWKEDGADPTPLDNNVLDRLKQFRAMNQFKKALRIIA 308  
322 ERLSEEEIGGLKELPKMIDTNSGTTTFEELKAGLRVGSSELMESIKSLMDAADIDNSG 381  
309 GCLSEEEITGLKEMFNKIDKNSGTTITLDELKHLAKHGPKLSDSEMELMEAADADGNG 368  
382 TIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSGYIITIDELQSACTEFGLCDT-PLDD 440  
369 LIDYDEFVTATVHMNKLDRHEHLHTAFQYFDKNSGYITKEELEHALKEQGLYDADKID 428  
441 MIKEIDLNDGKIDFSEFTAMMRKG 465  
429 IISDADSDNDGRIDYSEFVAMMRKG 453

## RESULT 12

US-08-459-444-22  
; Sequence 0, Application US/08459444A  
; Patent No. 6121014

## GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.

TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED  
NUCLEIC ACID CODING SEQUENCE

## NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:  
ADDRESS: No. 6121014artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,444A  
FILING DATE: 02-Jun-1995  
CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: /note= "derived protein sequence of

SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..464  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-08-459-444-22

Query Match 55.4%; Score 1437.5; DB 3; Length 464;

Best Local Similarity 60.9%; Pred. No. 8.4e-112; Mismatches 103; Indels 1; Gaps 1;

Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;

QY 22 LRHYLLGKLGQGGFGTTYLCTEKSTANYACKSIPKRLVCREDEYDVMREIQIMHHL 81

Db 9 VRATYSMGKELGRGQGVTHLCTHRTSGEKLAKTIAKEKLAAREDDVDDVREVOIMHHL 68

QY 82 SEHPNVVRIKGYEDSVFVHIVMEVCEGELFDRIVSKGHFSERBAVKLIKILGVVEAC 141

Db 69 SQQPNVVGIRGAYEDKQSVHLMELCAGGELFDRIIARGQYTERGAALLRAIVQIVHTC 128

QY 142 HSLGVNHRDLKPENFLSPKODAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPVLKK 201

Db 129 HSGVMVHRDLKPENFLSKDEADPLKATDFGLSVFKEGELLRDIVGSAYYIAPEVLKR 198

QY 202 CYGPEIDVNSAGVILYLLSGVPPFWAETESGIFROILOGLKLDKDFSDPMTTISEAAKDLI 261

Db 189 KYGPEADIVSGVMLYIFLAGVPPFWAENENGIFTAILRGQLDLSSEPWPHPISPGAKDLV 248

QY 262 YKMLERSPKKRISAHEALCHPWIVDQAAAPDKPLDPAVLRSRLKQFSOMNKIKKMLRVIA 321

Db 249 KQMLNINPKERLTAFQVLNHPWKEDGADPTPLDNNVLDRLKQFRAMNQFKKALRIIA 308

QY 322 ERLSEEEIGGLKELPKMIDTNSGTTTFEELKAGLRVGSSELMESIKSLMDAADIDNSG 381

Db 309 GCLSEEEITGLKEMFNKIDKNSGTTITLDELKHLAKHGPKLSDSEMELMEAADADGNG 368

QY 382 TIDYGEFLAATLHMNMKEREELVAAFSDFDKDGSGYIITIDELQSACTEFGLCDT-PLDD 440

Db 369 LIDYDEFVTATVHMNKLDRHEHLHTAFQYFDKNSGYITKEELEHALKEQGLYDADKID 428

QY 441 MIKEIDLNDGKIDFSEFTAMMRKG 465

Db 429 IISDADSDNDGRIDYSEFVAMMRKG 453

## RESULT 13

US-09-547-422-22  
; Sequence 0, Application US/09547422  
; Patent No. 6320100

## GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.  
Desai, Nalini M.  
Lewis, Kelly S.  
Kramer, Vance C.  
Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park



Db 61 QIVHTCHSMGVMRDILKPENFLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIA 120  
QY 196 PEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLKDFKSDPWPTISE 255  
Db 121 PEVLKRYGPEADIVSGVMLYIFLAGVPPFWAENENGIFTALRGQLDLSSEFPWPHISP 180  
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFQSNKNIKMM 315  
Db 181 GAKDLVKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRKQFRANMQFKA 240  
QY 316 ALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELSKSLMDAA 375  
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKGLAKHPKLSSEMEKLEMAA 300  
QY 376 DIDNSGTIDYGEFLAATLHMNMKMEREBILVAAFSDFDKDGSYITIDELQSACTEFGLCD 435  
Db 301 DADGNGLIDYDEFVTATVHMNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEQGLYD 360  
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465  
Db 361 ADKIKDIISDADSNDGRIDYSEFVAMMRKG 391

## RESULT 15

US-08-459-448A-21  
Sequence 21, Application US/08459448A  
Patent No. 5859336

## GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.  
APPLICANT: Desai, Nalini M.  
APPLICANT: Lewis, Kelly S.  
APPLICANT: Kramer, Vance C.  
APPLICANT: Warren, Gregory W.  
APPLICANT: Evola, Stephen V.  
APPLICANT: Crossland, Lyle D.  
APPLICANT: Wright, Martha S.  
APPLICANT: Merlin, Ellis J.  
APPLICANT: Launis, Karen L.  
APPLICANT: Rothstein, Steven J.  
APPLICANT: Bowman, Cindy G.  
APPLICANT: Dawson, John L.  
APPLICANT: Dunder, Erik M.  
APPLICANT: Pace, Gary M.  
APPLICANT: Suttie, Janet L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5859336artis Corporation  
STREET: Patent & Trademark Dept., 520 White Plains  
STREET: Rd., POB 2005  
CITY: Tarrytown  
STATE: New York  
COUNTRY: USA  
ZIP: 10591-9005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,448A  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Pace, Gary M.  
REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8582  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 408 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-459-448A-21

Query Match 49.3%; Score 1277.5; DB 2; Length 408;  
Best Local Similarity 61.9%; Pred. No. 1.5e-98;  
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;  
QY 76 QIMHHLSEHPNVRIKGTNYEDSVFVHVMVEVCGGELFDRIVSKGHSEAREAVKLIKITL 135  
Db 1 QIMHHLGGQPNVVGLRGAYEDKQSVHLVLMELCAGGELFDRIIARGQYTERGAALLRAIV 60  
QY 136 GVVEACHSLGVMRDLKPNFLFDSPKDDAKLAKATDFGLSVFVKPGQYLYDVVGSPPVVA 195  
Db 61 QIVHTCHSMGVMRDILKPENFLLLSKDEDAPLKATDFGLSVFFKEGELLRDIVGSAYYIA 120  
QY 196 PEVLKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFRQILQGLKDFKSDPWPTISE 255  
Db 121 PEVLKRYGPEADIVSGVMLYIFLAGVPPFWAENENGIFTALRGQLDLSSEFPWPHISP 180  
QY 256 AAKDLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFQSNKNIKMM 315  
Db 181 GAKDLVKMLNINPKERLTAFQVLNHPWIKEDGDAPDTPLDNVVLDRKQFRANMQFKA 240  
QY 316 ALRVIAERLSEEEIGGLKELFKMIDTNSGTITFEELKAGLKRVSSELSKSLMDAA 375  
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKGLAKHPKLSSEMEKLEMAA 300  
QY 376 DIDNSGTIDYGEFLAATLHMNMKMEREBILVAAFSDFDKDGSYITIDELQSACTEFGLCD 435  
Db 301 DADGNGLIDYDEFVTATVHMNKLDRHEHLYTAFQYFDKNSGYITKEELEHALKEQGLYD 360  
QY 436 T-PLDDMIKEIDLNDGKIDFSEFTAMMRKG 465  
Db 361 ADKIKDIISDADSNDGRIDYSEFVAMMRKG 391

Search completed: November 28, 2003, 10:36:55

Job time : 27 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: November 28, 2003, 10:35:37 ; Search time 259 Seconds  
(without alignments)  
352.507 Million cell updates/sec

Title: US-09-848-806-1  
Perfect score: 2593  
Sequence: 1 METKNPRRPSNTVLPYQTP.....KNLFNFIADAFGVDGKSD 495

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues  
Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

- Database : Published Applications AA:\*
- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep.\*
  - 2: /cgn2\_6/ptodata/2/pubpaa/FCI\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
  - 4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*
  - 5: /cgn2\_6/ptodata/2/pubpaa/US07\_NEW\_PUB.pep.\*
  - 6: /cgn2\_6/ptodata/2/pubpaa/FCIUS\_PUBCOMB.pep.\*
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  - 15: /cgn2\_6/ptodata/2/pubpaa/US10C\_PUBCOMB.pep.\*
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  - 18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2593	100.0	495	12	US-09-848-806-1
3	2458	94.8	501	12	US-10-289-172-3
4	2458	94.8	501	12	US-09-848-806-3
5	1927	74.3	463	11	US-09-988-462-25
6	1672.5	64.5	639	10	US-09-854-731-17
7	1509.5	58.2	549	9	US-09-828-313-39
8	1437.5	55.4	464	11	US-09-988-462-22
9	1277.5	49.3	408	11	US-09-988-462-21
10	849	32.7	597	9	US-09-828-313-38
11	829	32.0	623	10	US-09-854-731-4
12	826	31.9	625	10	US-09-854-731-18
13	800	30.9	576	10	US-09-854-731-19
14	591	22.8	499	12	US-10-354-358-88
15	587.5	22.7	317	11	US-09-935-464-36

16	587.5	22.7	317	15	US-10-125-835-36	Sequence 36, Appli
17	587.5	22.7	370	10	US-09-817-181-4	Sequence 4, Appli
18	587.5	22.7	370	12	US-09-769-970-19	Sequence 19, Appli
19	587.5	22.7	370	12	US-10-090-002-4	Sequence 4, Appli
20	587.5	22.7	370	12	US-10-204-041-10	Sequence 10, Appli
21	587.5	22.7	370	15	US-10-142-356-7	Sequence 7, Appli
22	587.5	22.7	370	15	US-10-300-828-4	Sequence 4, Appli
23	578.5	22.3	473	12	US-10-320-351-15	Sequence 15, Appli
24	578.5	22.3	473	12	US-10-116-275-153	Sequence 153, Appli
25	566.5	21.8	516	12	US-09-820-790-2	Sequence 2, Appli
26	566.5	21.8	542	12	US-09-820-790-4	Sequence 4, Appli
27	554	21.4	355	12	US-10-355-975-10	Sequence 10, Appli
28	554	21.4	357	15	US-10-024-036B-2	Sequence 2, Appli
29	543.5	21.0	556	14	US-10-096-960-4	Sequence 4, Appli
30	543	20.9	460	11	US-09-935-464-3	Sequence 3, Appli
31	543	20.9	460	15	US-10-125-835-3	Sequence 3, Appli
32	543	20.9	476	11	US-09-935-464-5	Sequence 5, Appli
33	543	20.9	476	15	US-10-125-835-5	Sequence 5, Appli
34	539	20.8	565	14	US-10-096-960-2	Sequence 2, Appli
35	538.5	20.8	326	10	US-09-817-181-2	Sequence 2, Appli
36	538.5	20.8	326	12	US-10-090-002-2	Sequence 2, Appli
37	538.5	20.8	326	15	US-10-300-828-2	Sequence 2, Appli
38	537	20.7	254	11	US-09-898-837A-38	Sequence 38, Appli
39	533.5	20.6	387	10	US-09-771-161A-188	Sequence 188, Appli
40	532.5	20.5	343	12	US-09-769-970-5	Sequence 5, Appli
41	530	20.4	295	11	US-09-988-462-23	Sequence 23, Appli
42	510.5	19.7	648	15	US-10-024-036B-5	Sequence 5, Appli
43	510.5	19.7	817	10	US-09-992-481-4	Sequence 4, Appli
44	510.5	19.7	817	12	US-10-434-034-4	Sequence 4, Appli
45	509	19.6	1431	12	US-10-352-684A-38	Sequence 38, Appli

ALIGNMENTS

RESULT 1  
US-10-289-172-1  
; Sequence 1, Application US/10289172  
; Publication No. US20030154504A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: Calcium Dependent Protein Kinase  
; FILE OF INVENTION: Polyptides as Regulators of Plant Disease Resistance  
; FILE REFERENCE: 00786/389002  
; CURRENT APPLICATION NUMBER: US/10/289,172  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/201,925  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-289-172-1

Query Match	100.0%	Score 2593	DB 12	Length 495
Best Local Similarity	100.0%	Pred. No. 2.9e-187	Mismatches 0	Indels 0
Matches 495	Conservative 0			Gaps 0
QY	1	METKNPRRPSNTVLPYQTPRLRDHYLLGKLGQGFQGTYYLCTEKSTSANVACKSIPIKR	60	
Db	1	METKNPRRPSNTVLPYQTPRLRDHYLLGKLGQGFQGTYYLCTEKSTSANVACKSIPIKR	60	
QY	61	KLVCREDYEDVWREIQIMHHLSEHPNVRIKGTYESVVFVHVMVECEGELFDRIVSKG	120	
Db	61	KLVCREDYEDVWREIQIMHHLSEHPNVRIKGTYESVVFVHVMVECEGELFDRIVSKG	120	
QY	121	HFSEAEVKLTKTLGVVEACHSLGVMRDLPENFLDPSPKDDAKLKATDGLSVFYKPK	180	
Db	121	HFSEAEVKLTKTLGVVEACHSLGVMRDLPENFLDPSPKDDAKLKATDGLSVFYKPK	180	
QY	181	GQYLDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFFWAEETSGIFQILQ	240	

Db 181 GOYLVDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240  
QY 241 GKLDKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300  
Db 241 GKLDKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300  
QY 301 SRLKQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360  
Db 301 SRLKQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360  
QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKWEREEILVAAPDFDKDGSYIT 420  
Db 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKWEREEILVAAPDFDKDGSYIT 420  
QY 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480  
Db 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480  
QY 481 NIADAFGVGDKSDD 495  
Db 481 NIADAFGVGDKSDD 495

## RESULT 2

US-09-848-806-1  
; Sequence 1, Application US/09848806  
; Publication No. US20030167516A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: Calcium Dependent Protein Kinase  
; TITLE OF INVENTION: Polypeptides as Regulators of Plant Disease Resistance  
; FILE REFERENCE: 00786/389002  
; CURRENT APPLICATION NUMBER: US/09/848,806  
; CURRENT FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 60/201,925  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 495  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-09-848-806-1

Query Match 100.0%; Score 2593; DB 12; Length 495;  
Best Local Similarity 100.0%; Pred. No. 2.9e-187;  
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 METKPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKR 60  
Db 1 METKPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKR 60  
QY 61 KLVCREYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSKG 120  
Db 61 KLVCREYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSKG 120  
QY 121 HFSEBAVKLIKTLGVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKP 180  
Db 121 HFSEBAVKLIKTLGVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKP 180  
QY 181 GOYLVDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240  
Db 181 GOYLVDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 240  
QY 241 GKLDKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300  
Db 241 GKLDKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 300  
QY 301 SRLKQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360  
Db 301 SRLKQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVG 360

QY 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKWEREEILVAAPDFDKDGSYIT 420  
Db 361 SELMESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKWEREEILVAAPDFDKDGSYIT 420  
QY 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480  
Db 421 IDELQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 480  
QY 481 NIADAFGVGDKSDD 495  
Db 481 NIADAFGVGDKSDD 495

## RESULT 3

US-10-289-172-3  
; Sequence 3, Application US/10289172  
; Publication No. US20030154504A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: Calcium Dependent Protein Kinase  
; TITLE OF INVENTION: Polypeptides as Regulators of Plant Disease Resistance  
; FILE REFERENCE: 00786/389002  
; CURRENT APPLICATION NUMBER: US/10/289,172  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/201,925  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 501  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-289-172-3

Query Match 94.8%; Score 2458; DB 12; Length 501;  
Best Local Similarity 94.8%; Pred. No. 4.4e-177;  
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;

QY 4 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKRKL 63  
Db 3 KPNRRPSNTVLPYQTPRLRDHYLLGKLGQGGQFGTTLCTEKSTSYACKSIPKRKL 62  
QY 64 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSKGHFS 123  
Db 63 CREDYEDVWREIQIMHHLSEHPNVVRIKGTYESVVFHIVMEVCEGELFDRIVSKGCF 122  
QY 124 EREAVKLIKTLGVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQY 183  
Db 123 EREAAKLIKTLGVVEACHSLGVNHRDLKPENFLDPSKDDAKLKATDFGLSVFYKPGQY 182  
QY 184 LYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 243  
Db 183 LYDVVGSPYYVAPEVLKCYGPEIDVWSAGVILYLLSGVPPFWAETESGIFRQILQ 242  
QY 244 DFKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 303  
Db 243 DFKSDPWPPTISEAAKDLIYKMLERSPKKRI SAHEALCHPWIVDEQAAPDKPLDPAVL 302  
QY 304 KQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSEL 363  
Db 303 KQFSQMNKI KKMALRVIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSEL 362  
QY 364 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKWEREEILVAAPDFDKDGSYITIDE 423  
Db 363 MESEIKSLMDAADIDNSGTIDYGEFLAATLHMNMKWEREEILVAAPDFDKDGSYITIDE 422  
QY 424 LQSACTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 483  
Db 423 LQQAQCTEFGLCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVGRSRTMMKNLNF 482  
QY 484 DAFGVGDKSDD 495  
Db 483 EAFGVGDKSDD 498

RESULT 4  
US-09-848-806-3  
; Sequence 3, Application US/09848806  
; Publication No. US20030167516A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: Calcium Dependent Protein Kinase  
; FILE REFERENCE: Polypeptides as Regulators of Plant Disease Resistance  
; CURRENT APPLICATION NUMBER: US/09/848,806  
; PRIOR FILING DATE: 2001-05-03  
; PRIOR APPLICATION NUMBER: US 60/201,925  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; TYPE: PRT  
; LENGTH: 501  
; ORGANISM: Arabidopsis thaliana  
; US-09-848-806-3

Query Match 94.8%; Score 2458; DB 12; Length 501;  
Best Local Similarity 94.8%; Pred. No. 4.4e-177;  
Matches 470; Conservative 9; Mismatches 13; Indels 4; Gaps 1;  
  
QY 4 KNPSPSTVLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTANSYACKSIPKRLV 63  
DB 3 KNPSPSTVLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTANSYACKSIPKRLV 62  
  
QY 64 CREDYEDVWREIQIMHLSHPNVRIKGYEDSVFVHLMVEVCEGGEFDRIVSKGHS 123  
DB 63 CREDYEDVWREIQIMHLSHPNVRIKGYEDSVFVHLMVEVCEGGEFDRIVSKGHS 122  
  
QY 124 EREAVKLKLTILGVVEACHSLGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQY 183  
DB 123 EREAVKLKLTILGVVEACHSLGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQY 182  
  
QY 184 LYDVVGSPPYVAPELVKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIPRQILQGL 243  
DB 183 LYDVVGSPPYVAPELVKCYGPEIDVWSAGVILYLLSGVPPFWAETSGIPRQILQGL 242  
  
QY 244 DFKSDPWTITSEAKDLIKMLERSPKRISAHEALCHPWIVDEQAAPKPLDPAVLSRL 303  
DB 243 DFKSDPWTITSEAKDLIKMLERSPKRISAHEALCHPWIVDEQAAPKPLDPAVLSRL 302  
  
QY 304 KQFSQMNKIKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITFEELKAGLKRVSSEL 363  
DB 303 KQFSQMNKIKKVALRVIAERLSEEEIGGLKELFKMIDTDSNGTITFEELKAGLKRVSSEL 362  
  
QY 364 MESEIKSLMDAADTNSGTIDYGEFLAATLHNMKMERBEILVAAPSDFKDGSYITIDE 423  
DB 363 MESEIKSLMDAADTNSGTIDYGEFLAATLHNMKMERBEILVAAPSDFKDGSYITIDE 422  
  
QY 424 LQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEPTAMMKRGDGVGRSRTMMKNLFNIA 483  
DB 423 LQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEPTAMMKRGDGVGRSRTMMKNLFNIA 482  
  
QY 484 DAFGVG-----EKSD 495  
DB 483 EAFGVEDTSSTAKSD 498

RESULT 5  
US-09-988-462-25  
; Sequence 25, Application US/09988462  
; Publication No. US20030046726A1  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.

Warren, Gregory W.  
Evola, Stephen V.  
Crossland, Lyle D.  
Wright, Martha S.  
Merlin, Ellis J.  
Lauais, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE  
NUMBER OF SEQUENCES: 94  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/988,462  
FILING DATE: 20-NOV-2003  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 09/547,422  
FILING DATE: 11-APR-2000  
APPLICATION NUMBER: US 08/459,504  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: S-188051  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 463 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: Protein  
LOCATION: 1..463  
OTHER INFORMATION: /note= "protein sequence for  
soybean CDPK as shown in Figure 34."  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-988-462-25

Query Match 74.3%; Score 1927; DB 11; Length 463;  
Best Local Similarity 78.7%; Pred. No. 4.1e-137;  
Matches 365; Conservative 49; Mismatches 48; Indels 2; Gaps 2;  
  
QY 14 VLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTANSYACKSIPKRLVCREYEDVWR 73  
DB 1 VLPYQTPRLRDHYLLGKLGQGFQGTTLCTEKSTANSYACKSIPKRLVCKEDYEDVWR 60  
  
QY 74 EIQIMHLSHPNVRIKGYEDSVFVHLMVEVCEGGEFDRIVSKGHSREAVKLK 133  
DB 61 EIQIMHLSHPNVRIKGYEDSVFVHLMVEVCEGGEFDRIVSKGHSREAVKLK 120  
  
QY 134 ILGVVEACHSLGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 193  
DB 121 ILGVVEACHSLGVWHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPY 180

Qy 194 VAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKSDPWPPTI 253  
Db 181 VAPEVLKLYCPESDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKSDPWPPTI 240  
Qy 254 SEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDPLDPAVLRLKQFSOMKIK 313  
Db 241 SDSAKDLIRKWLQDNPKTRTAHEVLRHPWIVDDNIAPDKPLDSAVLSRLKQFSAMNKLK 300  
Qy 314 KMLARVIAERLSEEEIGLKFELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 373  
Db 301 KMLARVIAERLSEEEIGLKFELFKMIDTNSGTTTFEELKAGLKRVSSELMSEIKSLMD 360  
Qy 374 AADIDNSGTTDYGEFLAATLHMNMKEREIEILVAAFSDPKDQSGYITIDELQSACTEFL 433  
Db 361 AADIDKSGTTDYGEFLAATLHMNMKEREIEILVAAFSDPKDQSGYITIDELQSACTEFL 420  
Qy 434 CDTPLDDMIKEIDLNDGKIDFSEFTAMRKGD-GVGRSRTMMK 476  
Db 421 DDHIDDDMIKEIDQNDGQIDYGEFAAMMRKNGGIGR-RTMRK 463

RESULT 6  
US-09-854-731-17  
; Sequence 17, Application US/09854731  
; Patent No. US20020120949A1  
; GENERAL INFORMATION:  
; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 17  
; LENGTH: 639  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-09-854-731-17

Query Match 64.5%; Score 1672.5; DB 10; Length 639;  
Best Local Similarity 66.3%; Pred. No. 9.3e-118;  
Matches 318; Conservative 66; Mismatches 83; Indels 13; Gaps 3;

Qy 5 PNPRPQVKRVSSAGLLGSLVLRKTENLKQKSLGRRLGQGFQGTTHLCVERATGKEL 179  
Db 120 PSRPRQVKRVSSAGLLGSLVLRKTENLKQKSLGRRLGQGFQGTTHLCVERATGKEL 179  
Qy 53 ACKSIPKRLVCRDIEDVWREIQIMHLSHNPVVRIGTYEDSVFVHIVMEVCEGGEL 112  
Db 180 ACKSILKRLGSDDDVEDVRREIQIMHLAGHPSVVGIRGAYEDAVAVHLVMEQLCGGEL 239  
Qy 113 FRIIVSKGHFSREAEVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDF 172  
Db 240 FRIIVRGHYTERKAELARVIGVVEACHSGMWHRDLKPNFLFADHSEEAALKTIDF 299  
Qy 173 GLSVFYKPGQYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETES 232  
Db 300 GLSIFRPGQIFTDVVGSPYVAPEVLKCYGPEADVMSAGVILYLLCGVPPFWAENDQ 359  
Qy 233 GFRQILQKLDKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPD 292  
Db 360 GIFEVLVHRLDFESEWPFSISDGAKDLVRRMLVRDPRKRLTAHEVLRHPWVQGVAPD 419  
Qy 293 KPLDPAVLRLKQFSOMKIKKMLARVIAERLSEEEIGLKFELFKMIDTNSGTTTFEEL 352  
Db 420 RPLDSAVLSRLKQFSAMNKLKMLARVIAERLSEEEIGLKFELFKMIDTNSGTTTFEEL 479  
Qy 353 KAGLKRVSSELMSEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKEREIEILVAAFSDPD 412  
Db 480 KVGLSEKVGANLQSEBIYALMQAADVNDNGTTIDYGEFLAATLHNVKVEREDHLFAAFQYFD 539

Qy 413 KQSGYITIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVCGRSR 472  
Db 540 KQSGYITIDELQSACTEFLGCDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGVCGRSR 598

RESULT 7  
US-09-828-313-39  
; Sequence 39, Application US/09828313  
; Patent No. US20020059662A1  
; GENERAL INFORMATION:  
; APPLICANT: COSTA e SILVA, OSWALDO DA  
; APPLICANT: BOHNERT, HANS J.  
; APPLICANT: THIELEN, NOCHA VAN  
; APPLICANT: CHEN ROUYING  
; APPLICANT: SARRIA-MILLAN, RODRIGO  
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
; FILE REFERENCE: 16313-0032  
; CURRENT APPLICATION NUMBER: US/09/828,313  
; CURRENT FILING DATE: 2001-04-06  
; PRIOR APPLICATION NUMBER: 60/196,001  
; PRIOR FILING DATE: 2000-04-07  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 39  
; LENGTH: 549  
; TYPE: PRT  
; ORGANISM: Physcomitrella patens  
US-09-828-313-39

Query Match 58.2%; Score 1509.5; DB 9; Length 549;  
Best Local Similarity 60.8%; Pred. No. 1.5e-105;  
Matches 290; Conservative 70; Mismatches 112; Indels 5; Gaps 3;

Qy 5 PNPRPSNT---VLPYQTPRLRDHYLLGKLGQGFQGTTYLCTEKSITSANYACKSIPKRR 61  
Db 69 PRPKPASRSVSGVLGKPLSDIRQSYILGRELGRQFGVYILCTDKMTNEAYACKSIKRR 128  
Qy 62 LYCREDIYDVWREIQIMHLSHNPVVRIGTYEDSVFVHIVMEVCEGGELFRIIVSKGH 121  
Db 129 LTSKEDIYDVWREIQIMHLSHNPVVRIGTYEDSVFVHIVMEVCEGGELFRIIVSKGH 121  
Qy 122 FSERAEVKLITLGVVEACHSLGVWHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPG 181  
Db 189 YSERAADMCVRIVNVVHRCHSLGVFHRDLKPNFLFDSPKDDAKLKATDFGLSVFYKPG 248  
Qy 182 QYLYDVVGSPPYVAPEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQ 241  
Db 249 DVFQDIVGSAYYVAPEVLKCYGPEADVMSAGVILYLLCGVPPFWAETEQGIFDAVLKG 308  
Qy 242 KLDKSDPWPPTISEAAKDLIYKMLERSPKKRISAHEALCHPWIVDQAAAPDPLDPAVL 301  
Db 309 HIDFENDPMPKISNGAKDLVRKMLNPNVKIRLTAQOVLNHPNMWKEDGADPDVPLDNAVLT 368  
Qy 302 RLKQFSOMKIKKMLARVIAERLSEEEIGLKFELFKMIDTNSGTTTFEELKAGLKRVS 361  
Db 369 RLKQFSOMKIKKMLARVIAERLSEEEIGLKFELFKMIDTNSGTTTFEELKAGLKRVS 428  
Qy 362 ELMESEIKSLMDAADIDNSGTTIDYGEFLAATLHMNMKEREIEILVAAFSDPKDQSGYIT 421  
Db 429 KLNESDIRKLEAADVNGKIDFNEFISATMNMKTEKEDHLMAAFMFHFDTDNSGYIT 488  
Qy 422 DELQSACTEFLGCD-TPLDDMIKEIDLNDGKIDFSEFTAMMRKGD-GVGRSRTMMK 476  
Db 489 DELOAMEKNGMDPETTIEIISVDTDNGRIDYDEFVAMMRKNGPGAENGCTVKNK 545

RESULT 8  
US-09-988-462-22  
; Sequence 22, Application US/09988462  
; Publication No. US20030046726A1  
; GENERAL INFORMATION:



QY	142	HSLGVMHRDLKPENFLFDSKPKDAKLKATDGLSVFYKPGQYLYDVVGVSPYYVAPEVLKK	201
Db	129	HSMGVMHRDIKPENFLLLSKXEDAPLAKATDGLSVFPKKEGELLRDIVGSAYYIAPEVLKR	188
QY	202	CYGPEDVWSAGVILYILLSGVPPFWAETESGIFRQILQOKLDFKSDPWPPTISEAAKDLI	261
Db	189	KYGPEDVWSAGVILYIFLAGVPPFWAENENGIFTALRGQLDLSSSEPPWHISPGAKDLV	248
QY	262	YKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLSRLKQFOSOMNKIKKMLARVIA	321
Db	249	KMLNINPKERLTAFQVNLHPWIKEDGDADPTPLDNLVLDRLKQFRAMNOFKKAALRIIA	308
QY	322	ERLSEEEIGGLKELFKMIDTNSCTITFEELKAGLKRVSSELMESEIKSLMDAADIDNSG	381
Db	309	GCLSEEBITGLKEMFKNIDKDNSCTITLDELKHGLAKHGPKLSDSEWKLMEAADGNG	368
QY	382	TIDYGEFLAATLHNKMERBEILVAAPSDFKDQSGYITIDELQSACTEFLGCDT-PLDD	440
Db	369	LIDYDEFVTATVHNKLDREEHLYTAFQYFDKDNSGYITKEELEHALKEOGLYDADKID	428
QY	441	MIKEIDLNDGKIDFSEFTAMMRKG	465
Db	429	IISDADSDNDGRIDYSEFVAMMRKG	453
RESULT 9			
US-09-988-462-21			
; Sequence 21, Application US/09988462			
; Publication No. US20030046726A1			
; GENERAL INFORMATION:			
; APPLICANT: Koziel, Michael G.			
; Desai, Nalini M.			
; Lewis, Kelly S.			
; Kramer, Vance C.			
; Warren, Gregory W.			
; Evola, Stephen V.			
; Crossland, Lyle D.			
; Wright, Martha S.			
; Merlin, Ellis J.			
; Launis, Karen L.			
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED			
INSECTICIDAL ACTIVITY IN MAIZE			
NUMBER OF SEQUENCES: 94			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Syngenta Biotechnology, Inc.			
STREET: 3054 Cornwallis Road			
CITY: Research Triangle Park			
STATE: NC			
COUNTRY: USA			
ZIP: 27709			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/09/988,462			
FILING DATE: 20-NO. US20030046726A1-2001			
CLASSIFICATION: <Unknown>			
PRIOR APPLICATION DATA:			
APPLICATION NUMBER: US 09/547,422			
FILING DATE: 11-APR-2000			
APPLICATION NUMBER: US 08/459,504			
FILING DATE: 02-JUN-1995			
APPLICATION NUMBER: US 07/951,715			
FILING DATE: 25-SEP-1992			
APPLICATION NUMBER: US 07/772,027			
FILING DATE: 04-OCT-1991			
ATTORNEY/AGENT INFORMATION:			
NAME: Meigs, J. Timothy			
REGISTRATION NUMBER: 38,241			
REFERENCE/DOCKET NUMBER: S-188051			
TELECOMMUNICATION INFORMATION:			
TELEPHONE: (919)541-8587			
TELEFAX: (919)541-8689			
INFORMATION FOR SEQ ID NO: 22:			
SEQUENCE CHARACTERISTICS:			
LENGTH: 464 amino acids			
TYPE: amino acid			
STRANDEDNESS: single			
TOPOLOGY: linear			
MOLECULE TYPE: protein			
HYPOTHETICAL: NO			
FEATURE:			
NAME/KEY: Protein			
LOCATION: 1..464			
OTHER INFORMATION: /note= "derived protein sequence of			
pollen specific CDPK as disclosed in Figure 34."			
SEQUENCE DESCRIPTION: SEQ ID NO: 22:			
US-09-988-462-22			
Query Match 55.4%; Score 1437.5; DB 11; Length 464;			
Best Local Similarity 60.9%; Pred. No. 3.2e-100;			
Matches 271; Conservative 70; Mismatches 103; Indels 1; Gaps 1;			
QY	22	LRHYLLGKGLGQGGTGYLCTEKTSANYACKSIPKPKLVCRDVEDVMEIQIMHHL	81
Db	9	VRATYSGVELGQGGVGHVLTCTHRTSGEKLACKIAKKLAAREDDVDVREQIMHHL	68
QY	82	SEHPNVIRKGYEDSVFVHIVMEVCEGGELFDRIVSKHFSEREAVKILKILGVBEAC	141
Db	69	SGQPNVVLGRGAYEDKQSVHLVWELCAGGELFDRIIARGQYTERGAELLRAIVQIVHTC	128

```
/
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 408 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-988-462-21

Query Match          49.3%; Score 1277.5; DB 11; Length 408;
Best Local Similarity 61.9%; Pred. No. 3.1e-88;
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 76 QIMHLSHPNVVRIKGTVEDSVFVHVMCEVCGGELFDRIVSKGHFSEREAVKLTKIL 135
Db 1 QIMHLSGQPNVVLGAGVDEKQSVHLVMELCAGGELFDRIIARGQYTERGAELRAIV 60

QY 136 GVVEACHSLGVMHRLDKPENFLFDSKDDAKLKATDFGLSVFYKPGQYLYDVVGSYYVA 195
Db 61 QIVHTCHSGVMVHRDIKPNFLLLSKDEDAPLKATDFGLSVFPFKEGELLRDIVGSAYIA 120

QY 196 PEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKSPWPTISE 255
Db 121 PEVLKCYGPEADIMSGVMVLYIFLAGVPPFWAENENGIFTAILRQGLDLSSEPPHISP 180

QY 256 AAKDLTKMLERSPKKRISAEALCHPWIVDEQAAPKPLDPAVLRLKQFSOMNKKM 315
Db 181 GAKDLVKMLNPNKRLTAQVNLHPWKEDGADPOTPLDNVVLRLKQFRAMNQFKKA 240

QY 316 ALRVIAERLSSEEIGGLKELFKMIDTNSGTITFEELKAGLKRGVSELMSEIKSLMDAA 375
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKHLAKHGPKLSDSEMEKLMEA 300

QY 376 DIDNSTIDYGFLEAFLAHMNMKEREELVAFSDFDKDGSVITIDELQSACTEFLGCD 435
Db 301 DADGNGLIDYDFVATVHMNKLDREELHYTAPQYFDKNSGSYITKEELEHALKEOGLYD 360

QY 436 T-PLDDMIKEIDLNDGKIDFSFTAMMRKG 465
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

RESULT 10
US-09-828-313-38
; Sequence 38, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNET, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 38
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Physcomitrella patens
US-09-828-313-38

Query Match          32.7%; Score 849; DB 9; Length 597;
Best Local Similarity 36.9%; Pred. No. 9.9e-56;
Matches 203; Conservative 92; Mismatches 163; Indels 92; Gaps 14;

/
/ TELEPHONE: (919)541-8587
/ TELEFAX: (919)541-8689
/ INFORMATION FOR SEQ ID NO: 21:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 408 amino acids
/   TYPE: amino acid
/   TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-988-462-21

Query Match          49.3%; Score 1277.5; DB 11; Length 408;
Best Local Similarity 61.9%; Pred. No. 3.1e-88;
Matches 242; Conservative 59; Mismatches 89; Indels 1; Gaps 1;

QY 76 QIMHLSHPNVVRIKGTVEDSVFVHVMCEVCGGELFDRIVSKGHFSEREAVKLTKIL 135
Db 1 QIMHLSGQPNVVLGAGVDEKQSVHLVMELCAGGELFDRIIARGQYTERGAELRAIV 60

QY 136 GVVEACHSLGVMHRLDKPENFLFDSKDDAKLKATDFGLSVFYKPGQYLYDVVGSYYVA 195
Db 61 QIVHTCHSGVMVHRDIKPNFLLLSKDEDAPLKATDFGLSVFPFKEGELLRDIVGSAYIA 120

QY 196 PEVLKCYGPEIDVMSAGVILYLLSGVPPFWAETESGIFRQILQKLDKSPWPTISE 255
Db 121 PEVLKCYGPEADIMSGVMVLYIFLAGVPPFWAENENGIFTAILRQGLDLSSEPPHISP 180

QY 256 AAKDLTKMLERSPKKRISAEALCHPWIVDEQAAPKPLDPAVLRLKQFSOMNKKM 315
Db 181 GAKDLVKMLNPNKRLTAQVNLHPWKEDGADPOTPLDNVVLRLKQFRAMNQFKKA 240

QY 316 ALRVIAERLSSEEIGGLKELFKMIDTNSGTITFEELKAGLKRGVSELMSEIKSLMDAA 375
Db 241 ALRIIAGCLSEEEITGLKEMFNKIDKNSGTITLDELKHLAKHGPKLSDSEMEKLMEA 300

QY 376 DIDNSTIDYGFLEAFLAHMNMKEREELVAFSDFDKDGSVITIDELQSACTEFLGCD 435
Db 301 DADGNGLIDYDFVATVHMNKLDREELHYTAPQYFDKNSGSYITKEELEHALKEOGLYD 360

QY 436 T-PLDDMIKEIDLNDGKIDFSFTAMMRKG 465
Db 361 ADKIKDIISDADSDNDGRIDYSEFVAMMRKG 391

RESULT 11
US-09-854-731-4
; Sequence 4, Application US/09854731
; Patent No. US20020120949A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/854,731
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/092,438
; PRIOR FILING DATE: July 10, 1998
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Oryza sativa
US-09-854-731-4

Query Match          32.0%; Score 829; DB 10; Length 623;
Best Local Similarity 40.6%; Pred. No. 3.3e-54;
Matches 183; Conservative 87; Mismatches 155; Indels 26; Gaps 11;

QY 26 YLLGKLGQGGQFGTTLCTEKSTSYN-----ACKSIKPKLVCFREDYEDVWREIQIMH 80
Db 172 YELCKEVRGHRGHGT--CSAVVKKEGKGVAVKIIAKAMTTAISIEDVRREVKILRA 229

QY 81 LSEHPNVVRIKGTVEDSVFVHVMCEVCGGELFDRIVSK-GHFSEREAVKLTKILGVVE 139
Db 230 LSGHNNLVKFDYDAGEDGLNVIVMCEVCGGELLDRILARGGRYTEEDAKAIVVQILSWA 289
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QY 140 ACHSLGVMHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 199  
DB 290 FCHLQGVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVL 349  
QY 200 KCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQGLKDPKSPDPWPTISEAAKD 259  
DB 350 HRSYSMEADWISGIVITVYLLCGSRPFWARTESGIFRSVLRADPNFDDSPWPTVSAEAKD 409  
QY 260 LLYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQWNKIKKQALRV 319  
DB 410 FVRFNLKDYKRMATAVQALTPWLDEQR--QIPDLILFRLVKQYLRLATPLKRLALKA 467  
QY 320 IAEELSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSELM--ESEIKSLMDAADID 378  
DB 468 LSKALREDELLYLKQFKLE--PRDGFVSLDNFRALTALTRYLTDAMKESRVLFLHALEPL 526  
QY 379 NSGTDYGEFLAATL---HNNKMER-BEILVAAFSDFDKGGXYITIDELQSACTEFGLC 434  
DB 527 AYRMDFEFCFAAISPYQLEALERWEEIAGTAFQFQEGNRRVISEEL---AOELNLA 583  
QY 435 DTP---LDDMIKEIDLNDGKIDFSEFTAMM 462  
DB 584 PHYSIVQDWIRK----SDGKLNFLGFTKFL 610

## RESULT 12

US-09-854-731-18  
; Sequence 18, Application US/09854731  
; Patent No. US20020120949A1  
; GENERAL INFORMATION:

; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 18  
; LENGTH: 625  
; TYPE: PRT  
; ORGANISM: Zea mays

US-09-854-731-18

Query Match 31.9%; Score 826; DB 10; Length 625;  
Best Local Similarity 40.8%; Pred. No. 5,7e-54;  
Matches 183; Conservative 85; Mismatches 159; Indels 22; Gaps 10;

QY 26 YLLGKGLGQGFQGTLYLCTEKS---TSANYACKSIPKRLKVCREDYEDVWREIQIMHLS 82  
DB 174 YDLGKEVGRGHGHTCSAVVKKGEHKGHTVAVKIISKAKMTTATISIEDVVRREVILKALS 233  
QY 83 BHPNVVRKGTVEDSVFVHIVMEVCEGGLFDRIVSK-GHFSEBAVKLIKTIILGVVEAC 141  
DB 234 GHDNLVRFYDACEALNVYIVMELCEGGLLRILARGGRYTEEDAIAIIVQILSVVAF 293  
QY 142 HSLGVMHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLCK 201  
DB 294 HLQGVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEVLHR 353  
QY 202 CYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQGLKDPKSPDPWPTISEAAKD 261  
DB 354 SYSMEADWISGIVITVYLLCGSRPFWARTESGIFRSVLRADPNFDDSPWPTVSAEAKD 413  
QY 262 KMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQWNKIKKQALRVIA 321  
DB 414 KRLNLDYKRMATAVQALTPWLDEQR--QIPDLILFRLVKQYLRLATPLKRLALKA 471  
QY 322 ERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSELM--ESEIKSLMDAADIDNS 380

DB 472 KALSEDELLYLRLQFKLE--PRDGFVSLDNFRALTALTRYLTRYSDAMRESRVLEFQHALEPLAY 530  
QY 381 GRIDYGEFLAATL---HNNKMER-BEILVAAFSDFDKGGXYITIDELQSACTEFGLC 436  
DB 531 RMDFEFCFAAISPYQLEALERWEEIAGTAFQFQEGNRRVISEEL---AOELNLA 587  
QY 437 P---LDDMIKEIDLNDGKIDFSEFTAMM 462  
DB 588 PHYSIVQDWIRK----SDGKLNFLGFTKFL 612

## RESULT 13

US-09-854-731-19  
; Sequence 19, Application US/09854731  
; Patent No. US20020120949A1  
; GENERAL INFORMATION:

; APPLICANT: Allen, Steve  
; APPLICANT: Lee, Jian Ming  
; TITLE OF INVENTION: Plant Protein Kinases  
; FILE REFERENCE: BB-1171  
; CURRENT APPLICATION NUMBER: US/09/854,731  
; CURRENT FILING DATE: 2001-05-14

; PRIOR APPLICATION NUMBER: 60/092,438  
; PRIOR FILING DATE: July 10, 1998  
; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: Microsoft Office 97  
; SEQ ID NO 19  
; LENGTH: 576  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana

US-09-854-731-19

Query Match 30.9%; Score 800; DB 10; Length 576;  
Best Local Similarity 38.1%; Pred. No. 4,6e-52;  
Matches 177; Conservative 94; Mismatches 171; Indels 22; Gaps 10;

QY 25 HYLKGLKGGQGFQGTLYLCTEKS---YACKSIPKRLKVCREDYEDVWREIQIMH 79  
DB 122 HYEIDGVEGRGHG--YTCASAKGKGLKQEVAVKVIKSKMTTATIAIEDVSREVKMLR 179  
QY 80 HLSEHPNVVRKGTVEDSVFVHIVMEVCEGGLFDRIVSK-GHFSEBAVKLIKTIILGVV 138  
DB 180 ALTGHNLVQFYDAFEDDENNVYIVMELCKGGLLQILQGGKYSDDAKVMVQILSVV 239  
QY 139 EACHSLGVMHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEV 198  
DB 240 AYCHLQGVHRDLKPNFLDPSKDDAKLKATDFGLSVFYKPGQYLYDVVGSPPYVAPEV 299  
QY 199 LKKCYGPEIDVMSAGVILYLLSGVPPFWAETSGIFRQILQGLKDPKSPDPWPTISEAAK 258  
DB 300 LHRTYGTADWMSIGVIAVILLCGRPFWARTESGIFRAVLKAEFPAEPWPSLSP 359  
QY 259 DLIYKMLERSPKKRISAHEALCHPWIVDEQAAPDKPLDPAVLRLKQFSQWNKIKKQALRV 318  
DB 360 DPKRLNLDYKRMATAVQALTPWLDEQR--QIPDLILFRLVKQYLRLATPLKRLALKA 418  
QY 319 VIAERLSEEEIGGLKELFKMIDTNSGTTITFEELKAGLKRVGSELM--ESEIKSLMDAAD 377  
DB 419 ALAKTLTPQALYLRQETTLGPGSKNGYISMONYKTAILKSDTDAMKOSRVDFVHMISC 478  
QY 378 DNGSDTYGEFLAATLHNNKMER---BEILVAAFSDFDKGGXYITIDELQSACTEFG 433  
DB 479 LQYKGLDPEEFECASALSVVQLEAMETWQHARRAYELFEKDNRRPIMIEELAS---ELGL 535  
QY 434 -CDTPLDDMIKEIDLNDGKIDFSEFTAMMRKGDGGRSRTMMK 476  
DB 536 GPSVPVHVVLQDWIRHNSDGLSFLGFLRLH---GVS-SRTLQK 575

## RESULT 14

US-10-354-358-88  
; Sequence 88, Application US/10354358  
; Publication No. US20030157082A1

```

; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc
; APPLICANT: Hunter, John Joseph
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Tsai, Fong-Ying
; APPLICANT: Lesoon, Andrea S.
; APPLICANT: Lightcap, Eric S.
; APPLICANT: Williamson, Mark
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 140, 1470, 1686, 2089, 2427, 3702, 5891, 6428,
; TITLE OF INVENTION: 7181, 7660, 25641, 69583, 49863, 8897, 1682, 17667, 9235,
; TITLE OF INVENTION: 3703, 14171, 10359, 1660, 1450, 18894, 2088, 32427, 2160,
; TITLE OF INVENTION: 9252, 9389, 1642, 85269, 10297, 1584, 9525, 14124, 4469,
; TITLE OF INVENTION: 8990, 2100, 9288, 64698, 10480, 20893, 32230, 1586, 9943,
; TITLE OF INVENTION: 16334, 68862, 9011, 14031, 6178, 21225, 1420, 32236, 2099,
; TITLE OF INVENTION: 2150, 26583, 2784, 8941, 9811, 27444, 50566 OR 66428 MOLECULES
; FILE REFERENCE: MP102-020P1RNONNIM
; CURRENT APPLICATION NUMBER: US/10/354,358
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: US 60/353,600
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 60/364,517
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/371,075
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: US 60/371,507
; PRIOR FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: US 60/372,984
; PRIOR FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US 60/374,194
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US 60/382,995
; PRIOR FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: US 60/385,023
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/388,853
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: US 60/389,395
; PRIOR FILING DATE: 2002-06-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-354-358-88

Query Match          22.8%; Score 591; DB 12; Length 499;
Best Local Similarity 37.1%; Pred. No. 2.2e-36;
Matches 142; Conservative 65; Mismatches 144; Indels 32; Gaps 9;

QY 21 RLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIPKRLKVCREDYEDVWREIOIMHH 80
Db 9 RTDEYQLVEELGKGAFSVVRCMK1PTGGYAAKIINTKKLSAR-DHOKLEREARIC-R 66

QY 81 LSEHPNVRIKGTYESVFIHVMVEYCEGGELFDRIIVSKGHFSEREAVKLIKILGWSEA 140
Db 67 LLKHPNIVRLHDSISEEGPHYLVDLVTGGELFDIVAREYYSSEADASHCIIQOILSVNH 126

QY 141 CHSLGVWHRDLKPFNLFDSPKDDAKLKATDGLSVFYKPGQYL-YDVVGSPPYVAPEVL 199
Db 127 CHLNGIVHRDLKPFNLLASKSGAAVKLADFLGLAEVQDQQAAMFGAGTGYLSPEVL 186

QY 200 KK-CYGPEDVWSAGVILYILLSGVPPFWAETESGIFROILOGKLDKSDPMTTISEAAK 258
Db 187 RKDPYKGPVDMWACGVILYILLGVPPFWDEQHRILQIKAGAYDFSPPEWDTVTPEAK 246

QY 259 DLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQNNKIKMALR 318
Db 247 DLINKMLTINPAKRITASEALKHPMICQSRSTVASMMHRQETVDCLCKFNAREKLG- -A 303
```

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QY 319 VIAERLSEERIGGLKELFKMID-----TONSG-TITFEELKA---GLKRVGSELMESEIK 369
Db 304 ILTTMLATRNFSAAKSLKKPKDGVCKESTESSNTTIEDVYKARKQEIIVKTEQLIEA--- 360
QY 370 SLMDAADIDNSGTIDYGEFLAAT 392
Db 361 -----INNGDFEAYT 370

RESULT 15
US-09-935-464-36
; Sequence 36, Application US/09935464
; Publication No. US20030027153A1
; GENERAL INFORMATION:
; APPLICANT: Meyer, Joanne
; APPLICANT: Barrington-Martin, Rory
; APPLICANT: Parker, Alexander
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCH
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
; FILE REFERENCE: 3322/1H702 US1
; CURRENT APPLICATION NUMBER: US/09/935,464
; CURRENT FILING DATE: 2001-08-23
; PRIOR APPLICATION NUMBER: US 09/757,300
; PRIOR FILING DATE: 2001-01-09
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 317
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-464-36

Query Match          22.7%; Score 587.5; DB 11; Length 317;
Best Local Similarity 41.6%; Pred. No. 2.3e-36;
Matches 124; Conservative 55; Mismatches 114; Indels 5; Gaps 4;

QY 18 QPRLRDHYLLGKLGQGGFTTYLCTEKSTSANVACKSIPKRLKVCREDYEDVWREIOI 77
Db 2 QAEDIRDIYDFRDVLGTGAFSEVILAEADKRTOKLVAIKIAKEALSGKEG--SMENEIAV 59

QY 78 MHHLSEHPNVRIKGTYESVFIHVMVEYCEGGELFDRIIVSKGHFSEREAVKLIKILGV 137
Db 60 LHKI-KHPNIVALDDIYESGGHLYLIMQLVSGELFDRIIVEKGYFTYERDASRLIFQVLDA 118

QY 138 VEACHSLGVWHRDLKPFNLFDSPKDDAKLKATDGLSVFYKPGQYLVDVVGSPYVAPE 197
Db 119 VKYLDHDLGIVHRDLKPFNLLYSLDEDSKIMISDFGLSKNEDPGSVLSTACGTPGYVAPE 178

QY 198 VL-KKCYGPEIDVWSAGVILYILLSGVPPFWAETESGIFROILOGKLDKSDPMTTISEA 256
Db 179 VLAQKPYSKAVDCWSIGVIAYILLCGYPPFYDENDAKLFEQILKAEYEFDSPYWDIDSDS 238

QY 257 AKDLIYKMLERSPKKRISAEALCHPWIVDEQAAPDKPLDPAVLSRLKQFSQNNKIKK 314
Db 239 AKDFIRHLMKEDPEKFRFTCEQALQHPWIAGDTAL-DKNIHQSVSEQIKKNFAKSKWKQ 295
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:37:02 ; Search time 5521 Seconds  
(without alignments)  
3667.862 Million cell updates/sec

Title: US-09-848-806-1  
Perfect score: 2593  
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Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues  
Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-DOCALLIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09848806 @CNG 1.1 3508 @runat\_28112003.103143.2335 -NCPU=6 -ICPU=3  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.sts.\*  
12: gb.sy.\*  
13: gb.un.\*  
14: gb.vi.\*  
15: em.ba.\*  
16: em.fun.\*  
17: em.hum.\*  
18: em.in.\*  
19: em.mu.\*  
20: em.om.\*  
21: em.or.\*  
22: em.ov.\*  
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27: em.sts.\*  
28: em.un.\*

RESULT 1

ALIGNMENTS

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34: em.htg.pin.\*  
35: em.htg.rod.\*  
36: em.htg.mam.\*  
37: em.htg.vrt.\*  
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39: em.htgo.hum.\*  
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41: em.htgo.other.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2593	100.0	1747	8	ATHCDPKB
2	2577	99.4	1488	6	AX506009 Sequence
3	2577	99.4	1519	8	AY113986 Arabidops
4	2577	99.4	1750	8	AY050981 Arabidops
5	2458	94.8	1657	8	ATU31752 Arabidops
6	2188	84.4	158096	8	AC007887 Genomic s
7	2087	80.5	197876	8	AL161831 Arabidops
8	2087	80.5	197394	8	AT161515 Arabidops
9	2064	79.6	1473	8	AY247755 Glycine m
10	2030	78.3	1754	8	GMU69173 Glycine m
11	1969.5	76.0	1732	8	AB051809 Solanum t
12	1944	75.0	1768	8	AX077706 Sequence
13	1944	75.0	1768	8	SOYCADPK
14	1937	74.7	1524	8	AY247754 Glycine m
15	1844.5	71.1	1473	6	AX506091 Sequence
16	1844.5	71.1	1693	8	ATACDPK9 Arabidops
17	1779.5	68.6	2126	8	AB042550 Oryza sat
18	1767	68.1	2439	6	AX653934 Sequence
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 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 REFERENCE 1 (bases 1 to 1747)  
 AUTHORS Urao,T., Katagiri,T., Mizoguchi,T., Yamaguchi-Shinozaki,K.,  
 Hayashida,N. and Shinozaki,K.  
 TITLE Two genes that encode Ca(2+)-dependent protein kinases are induced  
 by drought and high-salt stresses in Arabidopsis thaliana  
 JOURNAL Mol. Gen. Genet. 244 (4), 331-340 (1994)  
 MEDLINE 94359455  
 PUBMED 8078458  
 REFERENCE 2 (bases 1 to 1747)  
 AUTHORS Shinozaki,K.  
 TITLE Direct Submission  
 JOURNAL Submitted (30-OCT-1993) Kazuo Shinozaki, Tsukuba Life Science  
 Center, The Inst. of Physical and Chemical Res.; 3-1-1 Kohyadai,  
 Tsukuba, Ibaraki 350, Japan (E-mail:sinozaki@rtcs1.riken.go.jp,  
 Tel:0298-36-4359, Fax:0298-36-9060)  
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VERSION AX506009.1 GI:23387246
KEYWORDS Arabidopsis thaliana (thale cress)
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS Harper J.F., Kreps, J., Wang, X. and Zhu, T.
TITLE Stress-regulated genes of plants, transgenic plants containing
same, and methods of use
JOURNAL Patent: WO 0216655-A 704 28-FEB-2002;
The Scripps Research Institute (US) ; Syngenta Participations AG
(CH)
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DEFINITION Arabidopsis thaliana putative calcium-dependent protein kinase

ACCESSION AY113986

VERSION AY113986.1

KEYWORDS GI:21281140

SOURCE FLJ CDNA

ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (bases 1 to 1519)

AUTHORS Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Arabidopsis Open Reading Frame (ORF) Clones

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1519)

AUTHORS Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA

COMMENT The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAPL cDNAs (RAPL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the PUNI (ORF) clones using the RAPL cDNAs: Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers

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Query Match: 99.38% Indels: 0

DB: 8 Gaps: 0

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LOCUS  
DEFINITION Arabidopsis thaliana putative calcium-dependent protein kinase  
1750 bp mRNA linear PLN 18-SEP-2002

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
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REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
FEATURES  
source  
gene  
5'UTR  
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(Atlg35670) mRNA, complete cds.  
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AY050981.1 GI:15293094  
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Arabidopsis thaliana  
Arabidopsis thaliana  
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1 (bases 1 to 1750)  
Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,  
Goldsmith, A.D., Lee, J.M., Quach, H.D., Toriumi, M., Yu, G., Bowser, L.,  
Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,  
Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C.,  
Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M.,  
Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P.,  
Southwick, A., Tracy, S.E., Shinozaki, K., Davis, R.W., Ecker, J.R. and  
Theologis, A.  
Direct Submission  
Submitted (07-AUG-2001) Plant Gene Expression Center, 800 Buchanan  
Street, Albany, CA 94710, USA  
RIKEN Genomic Sciences Center (GSC) members carried out the  
collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN  
Arabidopsis Full-length cDNA'): Seki, M., Narusaka, M., Ishida, J.,  
Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J.,  
Hayashizaki, Y. and Shinozaki, K.  
The Salk, Stanford, PGEC (SSP) Consortium members carried out the  
sequencing and annotation of the RAFL cDNAs: Yamada, K., Liu, S.X.,  
Pham, P.K., Banh, J., Banno, F., Dale, J.M., Goldsmith, A.D.,  
Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.D., Tang, C.C.,  
Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Chen, H.,  
Cheuk, R., Jones, T., Karlin-Neumann, G., Kim, C., Koesema, E., Lam, B.,  
Lin, J., Meyers, M.C., Miranda, M., Nguyen, M., Palm, C.J., Shinn, P.,  
Southwick, A., Tracy, S.E., Davis, R.W., Ecker, J.R. and Theologis, A.  
Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to  
this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP/PGEC)  
contributed equally to this work as PIs.  
Annotation is based on the January 2002 version of the Arabidopsis  
genome submitted to GenBank.  
Location/Qualifiers  
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## RESULT 6

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 HTG AC007887.9 GI:8778333  
 KEYWORDS Arabidopsis thaliana (thale cress)  
 SOURCE Arabidopsis thaliana

ORGANISM  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsiis.

1 (bases 1 to 158096)

Ecker, J.R.

Direct Submission

TITLE Submitted (22-JUN-1999) Arabidopsis thaliana Genome Center,  
 JOURNAL Department of Biology, University of Pennsylvania, 38th Street and  
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA.

2 (bases 1 to 158096)

Ecker, J.R.

Direct Submission

TITLE Submitted (04-OCT-1999) Arabidopsis thaliana Genome Center,  
 JOURNAL Department of Biology, University of Pennsylvania, 38th Street and  
 Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA

3 (bases 1 to 158096)

Chou, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q.,

Johnson-Hopson, C., Khan, S., Kim, C., Altati, H., Bei, B., Chin, C.,  
 Chlou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,  
 Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J.,  
 Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H.,  
 Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M.,  
 Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J.

Direct Submission

TITLE Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,  
 JOURNAL Department of Biology, University of Pennsylvania, 38th and  
 Hamilton Walk, Philadelphia, PA 19104-6018, USA  
 COMMENT On Jun 28, 2000 this sequence version replaced gi:6007863.  
 This submission of BAC F1504 is shorter by 1338 bases. The  
 original BAC had a Tn10 transposon insertion  
 (gb|J01829.1|FN101813) from E. coli located at the junction of  
 bases 18229 and 18230 of this submission.

## FEATURES

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/evidence=not experimental

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/evidence=not experimental

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 97876)
AUTHORS McCombie,R.W., Spiegel,L.A., Huang,E.N., Nascimento,L.U., de la
Bastide,M., Vil,D.M., Preston,R.R., Matero,A., Shah,R.,
O'Shaughnessy,A., Rodriguez,M., Shekher,M., Schurz,K., See,L.H.,
Swaby,I., Habermann,K., Dedhia,N.N., Mewes,H.W., Lemcke,K. and
Mayer,K.F.X.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 97876)
AUTHORS EU Arabidopsis sequencing,project.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-2000) MIPS at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de
On Jun 22, 2000 this sequence version replaced gi:5916440.
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
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Query Match: 80.49% Indels: 383  
DB: 8 Gaps: 7

US-09-848-806-1 (1-495) x ATT25P22 (1-97876)

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Qy 124 GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer 143  
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RESULT 9
AY247755
LOCUS
DEFINITION
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ACCESSION
AY247755
VERSION
AY247755.1 GI:29892203
KEYWORDS
  Glycine max (soybean)
SOURCE
  Glycine max
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots;
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  Glycine.
REFERENCE
  1 (bases 1 to 1473)
  Tang, G.-Q., Dewey, R. and Huber, S.C.
  Biochemical characterization of calcium dependent protein kinase
  from Glycine max
JOURNAL
  Unpublished
REFERENCE
  2 (bases 1 to 1473)
  Tang, G.-Q., Dewey, R. and Huber, S.C.
  Direct Submission
AUTHORS
  Submitted (03-MAR-2003) Agricultural Research Service, US
JOURNAL
  Department of Agriculture, 3127 Ligon Street, Raleigh, NC 27607,
  USA
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 LOCUS  
 DEFINITION Glycine max calmodulin-like domain protein kinase isoenzyme beta  
 mRNA, complete cds.

ACCESSION U69173  
 VERSION GI:2501763  
 KEYWORDS calmodulin-like domain protein kinase; calcium-dependent  
 protein kinase.

SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 1754)  
 AUTHORS Lee,J.-Y., Roberts,D.M. and Harmon,A.C.  
 TITLE Isolation of two new CDPK isoforms (Accession Nos. U69173 and  
 JOURNAL U69174) from soybean (Glycine max L.) (PGR97-128)  
 REFERENCE 2 (bases 1 to 1754)  
 AUTHORS Lee,J.-Y., Yoo,B.-C. and Harmon,A.C.  
 TITLE Direct Submission

JOURNAL Submitted (03-SEP-1996) Botany, University of Florida, 220, Bartram  
 Hall, P.O. Box 118526, Gainesville, FL 32611, USA

FEATURES  
 Location/Qualifiers  
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US-09-848-806-1 (1-495) x GMU69173 (1-1754)

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ACCESSION AX077706
VERSION AX077706.1 GI:13122081
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ORGANISM Glycine max
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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Glycine.
1
REFERENCE
AUTHORS Holt,C.D., White,A.J., Michael,A.J. and Osborn,R.W.
TITLE Herbicide resistant plants and methods for the production thereof
JOURNAL Patent: WO 0107592-A 13 01-FEB-2001;
ZENECA LIMITED (GB)
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US-09-848-806-1 (1-495) x AX077706 (1-1768)
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 ORGANISM Glycine max  
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 Charbonneau H. and Harmon A.C.  
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 JOURNAL Science 252 (5008), 951-954 (1991)  
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VERSION AY247754.1 GI:29892112
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ORGANISM Glycine max
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Glycine.
REFERENCE 1 (bases 1 to 1524)
Tang,G.-Q., Dewey,R. and Huber,S.C.
Biochemical characterization of calcium dependent protein kinase
from Glycine max
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1524)
Tang,G.-Q., Dewey,R. and Huber,S.C.
Direct Submission
JOURNAL Submitted (03-MAR-2003) Agricultural Research Service, US
Department of Agriculture, 3127 Ligon Street, Raleigh, NC 27607,
USA
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REFERENCE Harper, J.F., Kreps, J.J., Wang, X. and Zhu, T.
AUTHORS Stress-regulated genes of plants, transgenic plants containing
TITLE same, and methods of use
JOURNAL Patent: WO 0216655-A 786 28-FEB-2002;
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US-09-848-806-1 (1-495) x AX506091 (1-1473)
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Db 1 ATGCGCAACAAACCAAGAACAGAG-----TGGGTTCCTTCTTCAAGACCCAAA 48
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Qy 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60
Db 109 TTCCTCTGTACCCATAAACACAGACAGGTCAAAAGCTTGCCTGCAATCCATACCCAAAAG 168
Qy 61 LysLeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHis 80
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Qy 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
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Qy 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
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Qy 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
Db 409 TGTCACTCTCTTGGTGTGTTCTAGAGATCTTAAACCTTGAGAAATTTCTTGTCTTCTCT 468
Qy 161 ProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
Db 469 TCTGATGAAGATGCTTCTCTTAAATCTACTGACTTTTGGCCTCTCTGTTTCTGCACACCA 528
Qy 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
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Qy 201 LysCysTyrGlyProGluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeu 220
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Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
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QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
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QY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
Db 1009 ACAGATAAAAGTGGGACTATCAGGTTGAAGAGTTAAAGATAGTAGTATGAGACGTGTTGGG 1068
QY 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
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QY 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysGlySerGlyTyrIleThr 420
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QY 478 LeuAsnPhe 480
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Search completed: November 28, 2003, 12:31:55

Job time : 5723 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:36:27 ; Search time 438 Seconds  
(without alignments)  
3050.735 Million cell updates/sec

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Perfect score: 2593  
Sequence: 1 METKNPRPSNTVLPYQTP.....KXNLFNIADAFVGDSKSD 495

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Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2593	100.0	1747	24	Arabidopsis CDPK2
2	2577	99.4	1498	24	Arabidopsis thalia
3	2458	94.8	1506	21	Arabidopsis thalia
4	2458	94.8	1657	24	Arabidopsis CDPK4
5	1944	75.0	1768	22	Soybean calcium de
6	1844.5	71.1	1473	24	Arabidopsis thalia
7	1762	68.0	2022	22	Vigna radiata calc
8	1742	67.2	1671	21	Arabidopsis thalia
9	1731	66.8	1635	24	Arabidopsis thalia
10	1724	66.5	1833	24	Arabidopsis thalia
11	1709.5	65.9	2550	22	Cucurbita pepo cal
12	1703	65.7	3054	21	Arabidopsis thalia
13	1586	61.2	2334	22	Rice calcium depen
14	1531.5	59.1	1647	22	Liverwort calcium
15	1524.5	58.8	1647	22	Liverwort calcium
16	1509.5	58.2	2230	24	Physcomitrella pat
17	1501	57.9	1332	21	Arabidopsis thalia
18	1484.5	57.3	2251	22	Tobacco calcium de
19	1482	57.2	2040	22	Rice calcium depen
20	1480	57.1	2306	22	Maize calcium depe
21	1462	56.4	1761	21	Arabidopsis thalia
22	1460.5	56.3	1723	22	Maize calcium depe
23	1458.5	56.2	2436	22	Soybean calcium de
24	1457	56.2	2466	15	Protein kinase cDN
25	1455	56.1	2363	22	Common ice plant c
26	1432.5	55.2	1791	22	Carrot calcium dep
27	1431	55.2	1910	22	Sweet potato calci
28	1381	53.3	1638	22	Arabidopsis thalia
29	1336	51.5	1967	22	Strawberry calcium
30	1325.5	51.1	1836	21	Arabidopsis thalia
31	1313.5	50.7	1602	24	Arabidopsis thalia
32	1313.5	50.7	1726	22	Arabidopsis thalia
33	1306	50.4	2162	22	Arabidopsis thalia
34	1225.5	47.3	2087	22	Arabidopsis thalia
35	1187.5	45.8	921	20	Arabidopsis thalia
36	1134	43.7	1082138	21	Tobacco CDPK cDNA.
37	1091	42.1	13114	21	Arabidopsis thalia
38	1049.5	40.5	1133	22	Rice gene for resi
39	1019.5	39.3	1781	21	Tobacco homolog of
40	985.5	38.0	2210	22	Arabidopsis thalia
41	950	36.6	956	22	Potato calcium dep
42	922.5	35.6	1412	21	Peanut calcium dep
43	887	34.2	1020	19	zea mays DNA fragm
44	887	34.2	1020	22	Nucleotide sequenc
45	857.5	33.1	1387	24	ATCDPK4a PK domain
					Physcomitrella pat

# ALIGNMENTS

RESULT 1  
ABA06021

ID ABA06021 standard; cDNA; 1747 BP.

XX ABA06021;  
AC ABA06021;

XX 08-MAR-2002 (first entry)

XX Arabidopsis CDPK2 encoding polynucleotide SEQ ID NO 2.

XX Arabidopsis; CDPK2; CDPK4; calcium dependent protein kinase; oilseed;  
KW disease resistance; agricultural; pathogen; crop yield; ornamental;  
KW fungicide; bactericide; nematocide; insecticide; viricide; cereal;  
KW transgenic; plant; enzyme; gene; ss.

XX Arabidopsis thaliana.

XX

FH Key Location/Qualifiers  
 FT CDS 67..1554  
 FT /\*tag= a  
 FT /product= "CDPK2"  
 XX  
 FN WO200184911-A1.  
 XX  
 PD 15-NOV-2001.  
 XX  
 XX  
 PF 04-MAY-2001; 2001WO-US14368.  
 XX  
 XX 05-MAY-2000; 2000US-201925P.  
 PR  
 XX (GEHO ) GEN HOSPITAL CORP.  
 PA  
 XX Sheen J;  
 PI  
 XX WPI; 2002-062179/08.  
 DR P-PSDB; AAM48000.  
 XX  
 XX Producing plant having increased disease resistance, comprises  
 PT regenerating plant from a non-naturally occurring plant cell  
 PT over-expressing a polynucleotide encoding a calcium dependent protein  
 PT kinase polypeptide -  
 XX  
 PS Disclosure; Fig 1; 44pp; English.  
 XX  
 CC The invention relates to producing a plant having increased disease  
 CC resistance, comprising providing a non-naturally occurring plant cell  
 CC over-expressing a polynucleotide encoding a calcium dependent protein  
 CC kinase (CDPK) polypeptide and regenerating a plant from the plant  
 CC cell, where the CDPK polypeptide is expressed in the plant, increasing  
 CC the resistance of the plant to disease as compared to a  
 CC naturally-occurring plant. The method is useful for a variety of  
 CC agricultural and commercial purposes, including improving a plant's  
 CC resistance against plant pathogens, increasing crop yields, improving  
 CC crop and ornamental quality and reducing agricultural production costs.  
 CC The method facilitates an effective and economical method for in-plant  
 CC protection against plant pathogen, reducing or minimising the need for  
 CC traditional chemical practices (e.g. application of fungicides,  
 CC bactericides, nematocides, insecticides or viciides) that are typically  
 CC used by farmers for controlling the spread of plant pathogens and  
 CC providing protection against disease causing pathogens. The method  
 CC contributes to the production of high quality and high yield agricultural  
 CC products, e.g. fruits, ornamentals, vegetables, cereals and field crops  
 CC having reduced spots, blemishes and blotches that are caused by  
 CC pathogens, agricultural products with increased shelf-life and reduced  
 CC handling costs and high quality and yield crops for agricultural  
 CC (e.g. cereal and field crops), industrial (e.g. oilseeds) and commercial  
 CC (e.g. fiber crops) purposes. The present sequence is that of Abrabidopsis  
 CC thaliana CDPK2 of the invention.  
 XX  
 SQ Sequence 1747 BP; 516 A; 316 C; 392 G; 523 T; 0 other;  
  
 Alignment Scores:  
 Pred. No.: 2,36e-245 Length: 1747  
 Score: 2593.00 Matches: 495  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 24 Gaps: 0  
  
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 DB 127 CGATTAAGAGATCATTAACCTTCTCGGAAAAAAGCTAGGCCAAGCCCAATTTGGAAACACC 186  
  
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187 TATCTCTGCACAGAGAAATCAACCTCCGCTAATTACGCTCGAATTCATCCGAGCGA 246  
 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMethHisHis 80  
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 141 CysHisSerLeuGlyValMetHisArgAspLysProGluAsnPheLeuPheAspSer 160  
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 161 ProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180  
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 201 LysCysTyrGlyProGluIleAspValTrpSerIleGlyValIleLeuTyrIleLeu 220  
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Qy 481 AsnIleLeuAspAlaPheGlyValAspGlyGluLysSerAspAsp 495  
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## RESULT 2

ABZ12899  
ID ABZ12899 standard; DNA; 1488 BP.

XX ABZ12899;

AC AC  
XX AC  
XX AC  
DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 704.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; da.

XX Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX W0200216655-A2.

PN 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

XX 22-JUN-2001; 2001US-300111P.

XX (SCRI ) SCRIPPS RES INST.

PA (SYGN ) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

PI WPI; 2002-304127/34.

XX Identifying a stress condition to which a plant cell has been exposed  
PT and producing plants with increased tolerance to these abiotic stresses  
PT -

PS Claim 144; SEQ ID NO 704; 577pp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides  
CC in the plant cell with an array or probes representative of the plant  
CC cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used  
CC in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed  
CC specification but is based on sequence information supplied to Derwent by  
CC the European Patent Office.

XX SQ Sequence 1488 BP; 443 A; 271 C; 365 G; 409 T; 0 other;

Alignment Scores:

Pred. No.: 7.16e-244 Length: 1488  
Score: 2577.00 Matches: 493  
Percent Similarity: 99.60% Conservative: 0  
Best Local Similarity: 99.60% Mismatches: 2  
Query Match: 99.38% Indels: 0  
DB: 24 Gaps: 0

US-09-848-806-1 (1-495) x ABZ12899 (1-1488)

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Db 1 ATGGAGACGAGCCAAACCCCTAGACGCTCTTCAAAACACAGTTCTACCATATCAACACCA 60  
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Qy 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60  
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Qy 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80  
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Qy 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 220  
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Qy 221 SerGlyValProPheThrAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240  
Db 661 AGCGGTGTCTCTCTCTCTGGGACAGACTGAGTCTGGAATCTTTAGACAGATATTGCA 720  
Qy 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaAlaLysAspLeu 260  
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Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280  
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Qy 281 HisProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300  
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Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320  
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OY 321 AlaGluArgLeuSerGluGluGluLeuGlyGlyLeuLeuGlyLeuPheLysMetIleAsp 340
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OY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
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OY 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
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OY 381 GlyThrIleAspTyrGlyGluPheLeuAlaIleThrLeuHisMetAsnLysMetGluArg 400
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OY 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
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OY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
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OY 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
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OY 461 MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe 480
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Db 1381 ATGATGAGGAAGGAGATGGAGTTGGGAGAGCAGACCAACCATGATGAAGAACTTGAACCTTC 1440
OY 481 AsnIleAlaAspAlaPheGlyValAspGlyGluLysSerAspAsp 495
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RESULT 3
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ID AAC44687 standard; DNA; 1506 BP.
AC AAC44687;
XX
XX 18-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 43752.
XX
XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
XX metabolic pathway; promoter; termination sequence; ss.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX 06-SEP-2000.
XX
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XX
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XX 20-JUL-1999; 99US-0144352.
XX 20-JUL-1999; 99US-0144632.
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XX 21-JUL-1999; 99US-0144814.
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PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
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PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 3,78e-232 Length: 1506
Score: 2458.00 Matches: 470
Percent Similarity: 96.57% Conservative: 9
Best Local Similarity: 94.76% Mismatches: 13
Query Match: 94.79% Indels: 4
DB: 21 Gaps: 1

US-09-848-806-1 (1-495) x AAC44687 (1-1506)

QY 4 LysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArg 23
Db 7 AAACCAAAACCCTAGAAAGACCCCTCAAAACAGTGTCTTCCATACGAACACCAAGATTAAAG 66
QY 24 AspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCys 43
Db 67 GATCACTATCTCTCGGCAAAAAGCTAGGCCAAGGCCAAATTGGAAACAACCTATCTCTGT 126
QY 44 ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal 63
Db 127 ACAGAGAAATCATCATCATGCTTAATACGCTTGCAATCAATCCCAACGATGAGCTTGA 186
QY 64 CysArgGluAspTyrGluAspValTrpArgGluLleGlnIleMetHisHisLeuSerGlu 83
Db 187 TGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTTCAGATCATGCATCATCTCTGAG 246
QY 84 HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal 103
Db 247 CATCCTAATGTGTAGAAATCAAGGGTACTTATGAAGACTCTGTGTTTGTTCACATGTT 306
QY 104 MetGluValCysGluGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer 123
Db 307 ATGGAAGTTTGTGAAGTGGTGAGCTTTTTCATCGGATGTTTCTAAAGGGGTGTTTAGT 366
QY 124 GluArgGluAlaValLysLeuLysThrIleLeuGlyValValGluAlaCysHisSer 143
Db 367 GAACGTGAAGCTGCTAAGTTTCATTAAAGACTATTCTGTGTGTTGTGAGGCTTGTCATTCT 426
QY 144 LeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp 163
Db 427 CTTGGTGTATGTCATAGAGATCTTAAGCCTGAGAAATTTCTTGTGATGATGATCCAGTGAT 486
QY 164 AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr 183
Db 487 GATGCTAAGCTTAAGCTACAGACTTTGGTTGTGCTTCTTCACAGCCAGGGCAGATAT 546
QY 184 LeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyr 203
Db 547 CTGTATGATGTAGTTGGAAGTCCGTAATATGTTGCACCTGAGGTTCTGAAAGAAATGTTAT 606
QY 204 GlyProGluLleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyVal 223
Db 607 GGACCAGAGATAGACGTGTGGAGCCGGTGTATCTTGTACATCTTACTAAGTGGGGTT 666
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QY	44	ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProGlyArgLysLeuVal	63
DB	127	ACAGAGAAATCATCATCAGCTAATTCAGCTTGCAATCAATCCCAAAACGTAAGCTTGTA	186
QY	64	CysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGlu	83
DB	187	TGTCGTGAAGACTACGAAGATGTATGGCGTGAGATTTCAGATCATCATCATCTCTCTCGAG	246
QY	84	HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal	103
DB	247	CATCCTAATGTTGTAGAAATCAAGGGTACTTATGAAGACTCTGTTTGTTCACATTGTT	306
QY	104	MetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer	123
DB	307	ATGGAAGTTGTGAAGGTGGTGAGCTTTTTCATCGAATGTGTTCTTAAAGGGTGTTTTAGT	366
QY	124	GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer	143
DB	367	GAACTGGAAGCTGCTTAAGTTGATTAAGACTATTCTTGGTGTGTGAGGCTTGTCAATCT	426
QY	144	LeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp	163
DB	427	CTTGCTGTATGCTAGAGATCTTAAGCCCTGAGAATTTCTTGTGTTGATAGTCCCACTGAT	486
QY	164	AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr	183
DB	487	GATGCTAAGCTTAAAGCTACAGACTTTGGTTGTCTGCTCTCTACAAGCCAGGGCAGTAT	546
QY	184	LeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyr	203
DB	547	CTGTATGATGATGTGGAAGTCCGTATTATGTGTGCACCTGAGGTCTCAAGAAATGTTAT	606
QY	204	GlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyVal	223
DB	607	GGACCAGAGATAGACGCTGTGGAGCGCGGTGTATCTTGTGTACATCTTACTAAGTGGGGTT	666
QY	224	ProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeu	243
DB	667	CCTCCTTTTGGGCAGAAACCGAGTCAGGAATCTTTAGCCAGATATTGCAAGGGGAAGATA	726
QY	244	AspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyrLys	263
DB	727	GATTTTAAATCTGATCCGTGCGCTACTATCTCAGAAGGTGCTAAAGAATTGATTTACAAA	786
QY	264	MetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrp	283
DB	787	ATGCTCGATAGAGCCCCAAGAAAGATTTTCTGCACATGAAGCATTTGTGTACCCCTTGG	846
QY	284	IleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeu	303
DB	847	ATTGTTGATGAACATGCTGTCACCAAGAGCTCTCGACCCAGCAGTCTTCTCGCGACTT	906
QY	304	LysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArg	323
DB	907	AAGCAGTTCTCGCAATGAATAAATCAAGAAATGGCCTTACCAGTAAATCGCGAGAGA	966
QY	324	LeuSerGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsn	343
DB	967	CTCTCGAGGAAGAGATGGTGGTCTGAAGGAAATGTTTCAAATGATAGATACAGACAC	1026
QY	344	SerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeu	363
DB	1027	AGTGGAAACAATCACCTTTGAAGAGCTTAAAGCAGGTCTTAAAGAGAGTTGGAATCT	1086
QY	364	MetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIle	383
DB	1087	ATGGAATCAGAAATCAAGTCTCTTATGGATGCGCGGATATAGACAAACAGTGGGACAATA	1146
QY	384	AspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluGluIle	403
DB	1147	GACTACGGTGAATTCCTTAGCAGCGACATTACATATAACAGATGGAGAGAGAGAGAAC	1206
QY	404	LeuValAlaAlaPheSerAspPheAspGlySerGlyTyrIleThrIleAspGlu	423

Db	1207	TTGGTGGTGGCGTTTTCATACTTTGATAAAGATGGTAGCGTTATATACCACTTGACGAG	1266
QY	424	LeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLys	443
Db	1267	CTTCAACAAGCCTGCACAGAGTTTGGTCTCTGTGACACTCCTCTTGATGCATGATCAAA	1326
QY	444	GlutAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArg	463
Db	1327	GAGATTGATCTTGTAATATGACGGGAGATTGATTTCTCAGAGTTTACTGCTATGATGAAG	1386
QY	464	LysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAla	483
Db	1387	AAAGCAGATGGTGTGGCAGGAGCAGAACTATGAGGAACAACCTTGAACCTTCAATATAGCT	1446
QY	484	AspAlaPheGlyValAspGly-----GlulysSerAspAsp	495
Db	1447	GAAGCTTTGGAGTTGAGGACACAAGCAGCACTGCTAAATCTCATGAT	1494
RESULT 5			
Id	AAF74274		
XX	AAAF74274 standard; DNA; 1768 BP.		
AC	AAAF74274;		
XX			
DT	04-MAY-2001 (first entry)		
XX			
DE	Soybean calcium dependent protein kinase clone #2.		
XX			
KW	Calcium dependent protein kinase; CDPK; herbicide resistance;		
KW	paraquat; diquat; crop production; ds.		
XX			
OS	Glycine max.		
XX			
PN	WO200107592-A2.		
FD			
PD	01-FEB-2001.		
XX			
PF	26-JUL-2000; 2000WO-GB02876.		
XX			
PR	27-JUL-1999; 99GB-0017642.		
XX			
PA	(ZENE ) ZENECA LTD.		
XX			
PI	Holt CD, White AJ, Michael AJ, Osborn RW;		
XX			
DR	WPI; 2001-168549/17.		
XX			
PT	Producing herbicide resistance plants by inhibiting calcium dependent		
PT	protein kinase in plants or by providing an intracellular vacuolar		
PT	transporter capable of transporting agrochemical into plant vacuole		
XX			
FS	Claim 18; Page 37; 50pp; English.		
XX			
CC	The present invention describes a method of producing plants which are		
CC	resistant to the herbicides paraquat and diquat, involving inhibiting in		
CC	the plants a calcium dependent protein kinase (CDPK) and selecting those		
CC	plants which are resistant to the agrochemical of interest. This is		
CC	useful in the production of crops with herbicide resistance.		
XX			
SQ	Sequence 1768 BP; 511 A; 325 C; 464 G; 468 T; 0 other;		
Alignment Scores:			
Pred. No.:	1.89e-181	Length:	1768
Score:	1944.00	Matches:	370
Percent Similarity:	88.45%	Conservative:	51
Best Local Similarity:	77.73%	Mismatches:	51
Query Match:	74.97%	Indels:	4
DB:	22	Gaps:	3
US-09-848-806-1 (1-495) x AAF74274 (1-1768)			
QY	14	ValLeuProTyrClnThrProArgLeuArgAspHisTyrLeuGlyValMetValClnGly	23





XX SQ Sequence 1473 BP; 438 A; 257 C; 365 G; 413 T; 0 other;

Alignment Scores:

Pred. No.:	9,22e-172	Length:	1473
Score:	1844.50	Matches:	353
Percent Similarity:	84.47%	Conservative:	55
Best Local Similarity:	73.08%	Mismatches:	68
Query Match:	71.13%	Indels:	7
DB:	24	Gaps:	2

US-09-848-806-1 (1-495) x ABZ12981 (1-1473)

QY 1 MetGluThrLysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrPro 20  
 DB 1 ATGGCGAACAAACAGAACAGACAG-----TGGGTTCCTTCAAGACCAAA 48

QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThr 40  
 DB 49 AACGTTGAAGACAACTACTTCTTGGTCAAGTCTTGGACACAGCCCAATTCGGNACCCT 108

QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60  
 DB 109 TTCCTCTGTACCCATAAACACAGACAGAGTCAAAAGCTTCGCTGCAAAATCCATACCAAAAGG 168

QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80  
 DB 169 AAGCTCTTGTCAAGAAAGATTACGACGCTTCTGAGAGAGATCCAGATAATGCAATCAC 228

QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100  
 DB 229 TTGCTGTAATACCCCAACGTTGTCGGTATAGAGAGTGGTACGAGGACCAAAACGCTG 288

QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120  
 DB 289 CATCTTGTGATGAGGCTTGTGAAGGAGGTGAGTGTGTTGATAGAAATGTTGAAGAGAGGT 348

QY 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140  
 DB 349 CATTACAGTGAAGAGAGAGCTGCTAAGCTTATCAAGACCAATTTGTGGGGTGTGAGGCG 408

QY 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160  
 DB 409 TGTCACTCTCTTGGTGTGTTTCATAGAGATCTTAAGCCTGAGAAATTTCTGTTTCTTCT 468

QY 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180  
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QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200  
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 DB 589 AAGCATTTATGGTCTCTGAATGTGACGTATGAGTGTGGAGTATCTCTACATCTCTTA 648

QY 221 SerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240  
 DB 649 TGTGGTTCCTTCCTTTTGGGCTGAGAGTGAATAAGGCATCTTTCAGGAAGATTTTACAG 708

QY 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaLysAspLeu 260  
 DB 709 GGAAGATGAGTTTGGAGATCAATCTTGGCCTAGCATTTTCAGAGAGTGCCAAAGATCTT 768

QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLysCys 280  
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 DB 829 CATCCGTGATGTGATGATGAAGTGTGCTCCAGATAAACCTTTGGACTGCGCGGTAGTG 888

QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320  
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QY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360  
 DB 1009 ACAGATAAAAGTGGGACTATCACGTTTGAAGAGTTAAAGATAGTAGACACGTGTTGGG 1068

QY 361 SerGluLeuMetGluSerGluLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380  
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QY 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400  
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QY 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460  
 DB 1309 ATGATCAAGAGCAATTCATCAAGATAATGATGGCAAAATAGACTATGGAGAAATTTGTGGCA 1368

QY 461 MetMetArgLysGlyAspGlyValGlyArgSer-----ArgThrMetMetLysAsn 477  
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QY 478 LeuAsnPhe 480  
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RESULT 7  
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 ID AAF74285 standard; DNA; 2022 BP.  
 XX  
 AC AAF74285;  
 XX  
 DT 04-MAY-2001 (first entry)  
 XX  
 DE Vigna radiata calcium dependent protein kinase clone.  
 XX  
 KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
 KW paraquat; diquat; crop production; ds.  
 XX  
 OS Vigna radiata.  
 XX  
 XX  
 XX WO200107592-A2.  
 XX  
 PD 01-FEB-2001.  
 XX  
 XX 26-JUL-2000; 2000WO-CB02876.  
 XX  
 PR 27-JUL-1999; 99GB-0017642.  
 XX  
 XX (ZENE ) ZENECA LTD.  
 XX  
 XX Holt CD, White AJ, Michael AJ, Osborn RW;  
 XX WPI; 2001-168549/17.  
 XX  
 XX Producing herbicide resistance plants by inhibiting calcium dependent  
 PT protein kinase in plants or by providing an intracellular vacuolar  
 PT transporter capable of transporting agrochemical into plant vacuole  
 XX

PS Claim 18; Page 44-45; 50pp; English.

CC The present invention describes a method of producing plants which are  
CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
CC plants which are resistant to the agrochemical of interest. This is  
CC useful in the production of crops with herbicide resistance.

XX Sequence 2022 BP; 587 A; 374 C; 466 G; 595 T; 0 other;

#### Alignment Scores:

Pred. No.:	1.87e-163	Length:	2022
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Percent Similarity:	82.19%	Conservative:	66
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US-09-848-806-1 (1-495) x AAF74285 (1-2022)

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Qy	44	rGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCy	64
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Qy	64	sArgGluAspTyrGluAspValTyrArgGluIleGlnIleMethHisLeuSerGluHi	84
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Qy	84	sProAsnValValArgLysGlyThrTyrGluAspSerValPheValHisIleValMe	104
Db	342	CAAGAACAATGTCACCAATTAAGGGTGTCTACAGGATCCTCTCTATGTGCATATAGTCAT	401
Qy	104	tGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGl	124
Db	402	GGAGCTTGTCTGGGGTGAGTTGTTGATCGCATCATCAGAGGGGCCATATACCGA	461
Qy	124	uArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLe	144
Db	462	GAGGAAGCTGCAGAGTTGACCAAAATATTGTTGGGGTGTTCAGGCTGTCTATTCCT	521
Qy	144	uGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAs	164
Db	522	TGGGGTCATGCACAGATCTCAAGCCAGAAAACTTTCTTTGGTCAATAAAGATGATGA	581
Qy	164	pAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLe	184
Db	582	TTTCTCTCTTAAGCAATGACTTTGGCTCTCCGTTTCTTCAAAACCCGGTCAAAATTTT	641
Qy	184	uTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGl	204
Db	642	CACGTGATGATGCGCAGCCCATACTATGTTGCTCTCTAGGTTCTCTCAAGCACTATGG	701
Qy	204	yProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPr	224
Db	702	GCCTGAAGCAGACGTGTGGACAGCCGGTGTACATCTGTACATATTGCTTAGTGGTACC	761
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Qy	244	pPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyrLysMe	264
Db	822	TTTTTGACTCAGATCTTGGCTCTAATATCTGACAGTGGAAAAAGATCTGATCAGAAAGAT	881
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Db	882	GCTGTGTTCTCAGCCTTCAGAACGTTGACTGCTCATCAAGTATTATGTCTATCTTGAT	941
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Qy	304	sGlnPheSerGlnMetAsnLysLysLysMetAlaLeuArgValIleAlaGluArgLe	324
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Qy	324	uSerGluGluGluIleGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSe	344
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KW	XX	protein identification; signal transduction pathway;	
KW	XX	metabolic pathway; promoter; termination sequence; ss.	
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Alignment Scores:
Pred. No.: 1,35e-161
Score: 1742.00
Percent Similarity: 82.12%
Best Local Similarity: 68.40%
Query Match: 67.18%
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US-09-848-806-1 (1-495) x AAC42924 (1-1671)

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QY 366 SerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyr 385
DQ 1309 ACAGAGATCCATGATCTTATGATGCGGCTGATGTAGACAAACAGTGGGACAATAGATTAC 1368
QY 386 GlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuVal 405
DQ 1369 AGTGAGTTCATTGCGCGGACGATCCATCTCAACAAACTAGAGCGGGAAGAGCATCTTGT 1428
QY 406 AlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGln 425
DQ 1429 GCAGCGTTTCAATATTTTGCACAAAGATGGAAGCGGTTTTCATAACAATTGATGAGTACAA 1488
QY 426 SerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIle 445
DQ 1489 CAAGCGTGTGTTGAACATGCGCATGGCTGATGTTTCTTGAAGACATCATCAAGAAGTT 1548
QY 446 AspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLysGly 465
DQ 1549 GATCAAAACAAATGATGGAAGATTTGATATGTTGAGTATGTTGGAGATGATGCAAAAGGA 1608
QY 466 Asp---GlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAlaAsp 484
DQ 1609 AATGCTGTTGTTGGAAGA---AGGACGATGAGAAATAGTCTAAACATTAGCATGAGAGAC 1665
QY 485 Ala 485
DQ 1666 GCG 1668

RESULT 9
AB214539
ID AB214539 standard; DNA; 1635 BP.
XX
AC AB214539;
```

XX 21-JAN-2003 (first entry)  
 XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2344.  
 XX Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
 XX Arabidopsis thaliana.  
 OS Arabidopsis thaliana.  
 XX WO200216655-A2.  
 XX 28-FEB-2002.  
 XX 24-AUG-2001; 2001WO-US26695.  
 XX 24-AUG-2000; 2000US-227866P.  
 PR 26-JAN-2001; 2001US-264647P.  
 PR 22-JUN-2001; 2001US-30011P.  
 XX (SCRI ) SCRIPPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX Harper JF, Kreps J, Wang X, Zhu T;  
 XX WPI; 2002-304127/34.  
 XX Identifying a stress condition to which a plant cell has been exposed  
 PT and producing plants with increased tolerance to these abiotic stresses  
 PT  
 XX Claim 144; SEQ ID NO 2344; 577pp + Sequence Listing; English.  
 XX The invention relates to identifying a stress condition to which a plant  
 CC cell has been exposed, comprising:  
 CC (a) contacting nucleic acid representative of expressed polynucleotides  
 CC in the plant cell with an array or probes representative of the plant  
 CC cell genome; and  
 CC (b) detecting a profile of expressed polynucleotides in the plant cell  
 CC characteristic of a stress response. The method is useful in the  
 CC production of transgenic plants, cells and seeds and in producing plants  
 CC with increased tolerance to abiotic stress. The present sequence is that  
 CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
 CC in methods of the invention.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification but is based on sequence information supplied to Derwent by  
 CC the European Patent Office.  
 XX  
 SQ Sequence 1635 BP; 474 A; 283 C; 393 G; 485 T; 0 other;  
 Alignment Scores:  
 Pred. No.: 1.59e-160 Length: 1635  
 Score: 1731.00 Matches: 328  
 Percent Similarity: 81.88% Conservative: 65  
 Best Local Similarity: 68.33% Mismatches: 85  
 Query Match: 66.76% Indels: 2  
 DB: 24 Gaps: 2  
 US-09-848-806-1 (1-495) x AB214539 (1-1635)  
 QY 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25  
 DB 193 AACGTTGACNATCAATCTTACTATGTTCTTGGTCACAAAGACTCCTAACATTCGTGATCTT 252  
 QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCysThrGlu 45  
 DB 253 TACACGTTGAGTCGTAAGTTAGCAAGGACAAATTCGGGACACGTAATTGTGTACTGAT 312  
 QY 46 LysSerThrSerAlaSerTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65  
 DB 313 ATTGCCACACGGTGTTCAGCTATGCTTGAAGTCTATATCCAAAGAGGAAATTTGATATCTAAA 372  
 QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGluHisPro 85  
 DB 1152

DB 373 GAAGATGTTGAGGATGTTAGGAGGAGATTTCAGATTATGCATCATTTAGCTGGTCACAAG 432  
 QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105  
 DB 433 AATATTGTTACTATTAAAGGAGCTTATGAGATCCTTTGTATGTTACATTTGTATGAGG 492  
 QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125  
 DB 493 CTTTGTGCTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 552  
 QY 126 GluAlaValLysLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145  
 DB 553 AAAGCTGCTGAGTTGACCAAGATCATTGTCGGTGTGTTGAGGCGTGTTCATCTCTGGT 612  
 QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165  
 DB 613 GTTATGCATAGAGATTTAAAGCCCTGAGAAATTTCTTGTGTTAATAGGATGATGATTC 672  
 QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185  
 DB 673 TCTCTTAAGCCATTGATTTTGGTCTCTCTGTTTCTTCAACCCAGGCCAAATATTCAAG 732  
 QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205  
 DB 733 GATGTTGTTGAAAGTCCATATGTTGCTCTCTGAGGTCTCTTCTTAAACCATTTATGTC 792  
 QY 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValPro 225  
 DB 793 GAAGCTGATGTGGACTGCTGGTGTATCTATCTTACTTAAGTGGTGGTGGTGGTGGTGGT 852  
 QY 226 PheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe 245  
 DB 853 TTCTGGCAGAAACACACAGCAAGGAATATTGATGCTGTGTTGAAGGGATATATTGACITT 912  
 QY 246 LysSerAspProTrpProThrIleSerGluAlaLysAspLeuIleTyrLysMetLeu 265  
 DB 913 GATACAGACCGTGGCCTGTCTATATCCGACAGTCTAAAGATCTGTATCCGGAAGATGTA 972  
 QY 266 GluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrpIleVal 285  
 DB 973 TGCTTAGTCTCTTCTGAACTGTTGACGTCTCATAGTCTTGCCTCATCTCCATGATCTGT 1032  
 QY 286 AspGluAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGln 305  
 DB 1033 GAGAAATGGAGTTGCACCGGATAGAGCACTTTGACCCGCTGTTTGTCTCGTCTAAACAG 1092  
 QY 306 PheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLysSer 325  
 DB 1093 TTTTCTGCAATGAATAAATTTAAAGAGATGGCTTTAAAGGTGATAGCTGAGAGCTCTCA 1152  
 QY 326 GluGluGluIleGlyGlyLeuLysGluPheLysMetIleAspThrAspAsnSerGly 345  
 DB 1153 GAAGAGAGATTCGGGTTTAAGAGCNAATGTTGAGGCAATGAGATCTGATAACGCGGT 1212  
 QY 346 ThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGlu 365  
 DB 1213 GCAATCAGCTTTGATGAACCTCAAAGCTGGCTTGAGAAAGATATGGATCAACCTTGAAGAC 1272  
 QY 366 SerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyr 385  
 DB 1273 ACCGAGATCCGAGATCTTATGGAAGCGGCTGATGTGGACAAACGCGGTACCAATAGATTAC 1332  
 QY 386 GlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuVal 405  
 DB 1333 AGCGAGTTTATTCACGCGAGCTCCATCTGAATAAAGTAGAGAGAGAGAGATCTTGTGTC 1392  
 QY 406 AlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGln 425  
 DB 1393 TCTGCAATTCAGTACTTTGACAAAGATGGAAGTGGTTACATCACCATTGATGAGCTCAA 1452  
 QY 426 SerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIle 445  
 DB 1453 CAATCTTGCAATGAATGGGATGACCGGATGTTTCTTGAAGACATAATCAAAAGATA 1512

QY 446 AspLeuAspAsnAspGlyValSerPheSerGluPheThrAlaMetMetArgIysGly 465  
 DB 1513 GATCAAGACACGATGGACGGATTGATTACGAAGAATTTGTCGATGATGCAAAAGGGA 1572  
 QY 466 Asp---GlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIleAlaAsp 484  
 DB 1573 AATGCTGCTGATAGGAGA--AGAACATGAATAATAGTCTAAACATCAGCATGAGAGAT 1629

## RESULT 10

ID ABZ14529 standard; DNA; 1833 BP.

AC ABZ14529;

DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 2334.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

KW Arabidopsis thaliana.

OS Arabidopsis thaliana.

XX WO200216655-A2.

PD 28-FEB-2002.

XX 24-AUG-2001; 2001WO-US26685.

XX 24-AUG-2000; 2000US-227866P.

PR 26-JAN-2001; 2001US-264647P.

PR 22-JUN-2001; 2001US-300111P.

XX (SCRI ) SCRIPPS RES INST.

PA (SYNG ) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

PS Claim 144; SEQ ID NO 2334; 577pp + Sequence Listing; English.

CC The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

CC (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

CC (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the

CC production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ14529-ABZ17574) used in methods of the invention.

CC Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

XX SQ Sequence 1833 BP; 545 A; 346 C; 486 G; 456 T; 0 other;

## Alignment Scores:

Pred. No.:	9.04e-160	Length:	1833
Score:	1724.00	Matches:	329
Percent Similarity:	77.89%	Conservative:	62
Best Local Similarity:	65.54%	Mismatches:	91
Query Match:	66.49%	Indels:	20
DB:	24	Gaps:	2

US-09-848-806-1 (1-495) x ABZ14529 (1-1833)

QY	2	GluThrLysPro-----AsnProArgArgPro-----	10
DB	316	GAGACCAAGCGGAGTCAAAACCTGATCCTCAGCTAAACCTAAGACCTAAACACACATG	375
QY	11	-----SerAsnThrValLeuProTyrGlnThrProArg	21
DB	376	AAGAGAGTGTCAGGTGCGAGGCTTAGGACTGAGTCAGTGTTCGAGAGGAGACTGAAAC	435
QY	22	LeuArgAspHisTyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrThrTyr	41
DB	436	TTCAAGGAATTTCTATTCCTTGGGAAGAACTCGGACAAAGGCAATTTGGGACGACTTTT	495
QY	42	LeuCyThrThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLys	61
DB	496	TTATGTGTCGAGAAGACTACCGGGAAGAGATTTCCTCGCAAGTCGATTCCTAAGAGAG	555
QY	62	LeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeu	81
DB	556	CTATTGACTGATGAGGACGTTGAGGATGTGAGAGAGAGAAATTCAGATAATGCATCATTG	615
QY	82	SerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHis	101
DB	616	GCTGGTCACCCCTAATGTCTCATCAAGGAGGCTTATGAGGATGTTGTGCGCAGTCAC	675
QY	102	IleValMetGluValCysGluGlyGlyLysLeuPheAspArgIleValSerLysGlyHis	121
DB	676	CTTGTATGAGGATGTTGTGCGGCGGCGAGCTTTTGACAGATCAATTCACACGCGGTGAC	735
QY	122	PheSerGluArgGluAlaValLysLeuLysThrIleLeuGlyValValGluAlaCys	141
DB	736	TACACAGAGAGAAAGCGGCTGAGCTCCTAGAACCATTTGTTGGGTTGTAGAGCTTGC	795
QY	142	HisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerPro	161
DB	796	CATTCTCTTGGTGTATGTCATCGAGACCTCAAGCCGAGAAATTTCTGTTGTCTAGTAA	855
QY	162	LysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGly	181
DB	856	CACGAGATTCCTCTTGAAGACGATGATTTTGAGCTCTCCATGTTCTTTAAACACGAC	915
QY	182	GlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLys	201
DB	916	GATGTTTTTACAGATGTTGTTGGTAGCCCATATTATGTTGCCAGAAATTTCTTCGAAAG	975
QY	202	CysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSer	221
DB	976	CGTTATGCGCCTGAAAGCTGATGCTGGAGTGTCTGGAGTGTGTGTATATTATTATTAAG	1035
QY	222	GlyValProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGly	241
DB	1036	GGAGTTCTCTCATTTCTGGGCTGAAACCGAACAGGTATTTTCGACACAGGTCTCTCACCGT	1095
QY	242	LysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIle	261
DB	1096	GATCTTGACATTTTCGTCGATCCCATGCAAGTATATCTGAAGTGAAGGATTTAGTG	1155
QY	262	TyrLysMetLeuGluArgSerProLysArgIleSerAlaHisGluAlaLeuLysCysHis	281
DB	1156	AGGAAATGCTGTGACGGATCCCAAGAAAGGTTAACTGCCCAAGTATTATTGTGAT	1215
QY	282	ProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSer	301
DB	1216	CCATGGGTTCAAGTCGACGGTGTGGCTCCAGACAGGCTTTGGATTCTGCTGTTCTGAGC	1275
QY	302	ArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAla	321
DB	1276	CGTATGAAGCAGATTTTCTGCAATGAACAAGTTCGAAGAAATGGCTCTTAGAGTATTGCT	1335
QY	322	GluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThr	341
DB	1336	GAGAGCTTATCTGAAGAAGAAATCGCGGCTTGAAGAAGAAATGTTTAAATATGATAGTGC	1395
QY	342	AspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySer	361



[illegible]

RESULT 11

RESOLUTION  
AAF74283

AAF74283  
ID AAF74283 standard; DNA; 2550 BP.

XX  
XX

AC AAF74283;

XX  
XX  
[continued on next page]

DT 04-MAY-2001 (first entry)

XX

DE Cucurbita pepo

XX

Calcium dependent

kw paraquat; diquat; crop produ  
yy

[illegible]

OS Cucurbita pepo.  
XX

XX  
PN  
W02C0107592-22

FN WOZC010/592-AZ.  
XX

XX PD 01-FEB-2001

FD 01-FEB-2001.  
XX

26-JUL-2000: 2000WO-GB02876.

XX  
20-00T-2000; 2000W-GB0Z878.

PR 27-JUL-1999; 99GB-0017642.

[illegible]

PA (ZENE) ZENECA LTD.

XX

PI Holt CD, White AJ, Michael AJ, Osborn RW;

XX

Alignment Scores:			
Pred. No.:	3.77e-158	Length:	2550
Score:	1709.50	Matches:	321
Percent Similarity:	80.61%	Conservative:	78
Best Local Similarity:	64.85%	Mismatches:	79
Query Match:	65.93%	Indels:	17
DB:	22	Gaps:	3
US-09-848-806-1 (1-495)	X	AAF74283 (1-2550)	

Qy	4	LysProAsnProArg-----ArgPro-----	10
Db	804	AAACCAAGAACCGCTATGGAAACCAGAGGTGCGCCCTGTTATGAAGAGGGTGGTAGTGCT	863
Qy	11	-----SerAsnThrValLeuProTyGlnThrProArgLeuArgAspHisTyLeu	27
Db	864	GGGCTTCGAGGTGGTTCCTCATAGACGAAACGGGAAACTTTAAGGAGTATTATAGC	923
Qy	28	LeuGlyLysLysLeuGlyGlnPheGlyThrThrTyrlLeuCysThrGluLysSer	47
Db	924	TTGGTAAAAAATTAGGCCAAGCACAAATTGGGCACAACATATATGTGTGTGGAGAAGGCA	983
Qy	48	ThrSerAlaAsnTyralaCysLysSerIleProLysArgLysLeuValCysArgGluAsp	67
Db	984	ACTGGGAAGAGATGCTGTGTAAGTCTATTGCAAAGAGGAAGTTGGTTAATAGGAGTAT	1043
Qy	68	TyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGluHisProAsnVal	87
Db	1044	GTTGNAGATGTGAGAGGGNAATTCAGATAATGCACCATTTGTCTGGACACCCGAATGTT	1103
Qy	88	ValArgIleLysGlyThrTyrlGluAspSerValPheValHisIleValMetGluValCys	107
Db	1104	ATATCATCAAGGGGGCTACGAGGATGCCGTTGCCAGTTCAGGTAGTCATGGAGTTGTGT	1163
Qy	108	GluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGluAla	127
Db	1164	GCTGGAGGTGAGCTATTGTATAGATCATTTCAACCTGGAGCATTTATACCGAAAGAAAGGCT	1223
Qy	128	ValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMet	147
Db	1224	GCTGAGCTTACTAGGACCATAGTCGGGGTTTTGGAGGCATGTCACGCTCTTCGAGTTATG	1283
Qy	148	HisArgAspLeuLysProGluAnPheLeuPheAspSerProLysAspAspAlaLysLeu	167
Db	1284	CACCGTGACCTTAAGCCCCGAGAAATTTTCTCTTTGTAGCAAGGAAGGAATCACCTCTC	1343
Qy	168	LysAlaThrAspPheGlyLeuSerValPheTyrlLysProGlyGlnTyrlLeuTyrlAspVal	187
Db	1344	AAGACAATTTGATTTGGACTATCAATGTCTTCAACACGAGCGAAAAGTTAATGATGTG	1403
Qy	188	ValGlySerProTyrlTyrValAlaProGluValLeuLysLysCystTyrlGlyProGluIle	207
Db	1404	GTCCGAGGTCCGTACTATGTTGCACCTGAAGTTTTTCGGAAGGCATATGCTCCAGAAGCA	1463
Qy	208	AspValTrpSerAlaGlyValIleLeuTyrlLeuLeuSerGlyValProProPheTrp	227
Db	1464	GATGTTTGAGTGCTGGAGTAATTGTATACATCTGTTAAGTGGAGTGCCTCCCTTTGG	1523
Qy	228	AlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPheLysSer	247
Db	1524	GCTGAGTCTGAGGAAGGATATTTGAAGAGGTCCTGCACGGCGCATCTTGACCTCTCTCC	1583
Qy	248	AspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyrlLysMetLeuGluArg	267
Db	1584	GACCCCTGGCCCAGCATCTCCGACATGCGAAAGATTTTGGTTAGAAGAAATGCTGTTCGA	1643
Qy	268	SerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrpIleValAspGlu	287
Db	1644	GACCCGAGAAAGAGACTGACACATATGAAGTTTTGTGCCACCTTGGGTTCAGTTGAT	1703
Qy	288	GlnAlaLaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSer	307



Ds	1704	GGTGTGCTCTGACAAAGCCGCTTGACTCGGCAGCTCTTGACTCGCTTGAAGCAGCTTTTCA	1763	PR	23-APR-1999;	99US-0130891.
Qy	308	GlnMetAsnIleLysLeuMetAlaLeuArgValIleAlaGluArgLeuSerGluGlu	327	PR	28-APR-1999;	99US-0131449.
Ds	1764	GCCATGAACAGCTCAAGAAATGGCTATCAAGGTCTATTCAGAGAGCTTATCTGAAGAA	1823	PR	30-APR-1999;	99US-0132048.
Qy	328	GluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIle	347	PR	04-MAY-1999;	99US-0132407.
Ds	1824	GAATTCCTGGACTCAAGGAATGTTCAAGATGATAGTACTGACACAGCGGCAATC	1893	PR	05-MAY-1999;	99US-0132484.
Qy	348	ThrPheGluLeuLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGluSerGlu	367	PR	06-MAY-1999;	99US-0132485.
Ds	1884	ACATTTCAAGAACTCAAGCTGGATTTGAAAAGTTTGGAGCTAATCTTAAGGAGTCCGAA	1943	PR	06-MAY-1999;	99US-0132486.
Qy	368	IleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyrGlyGlu	387	PR	07-MAY-1999;	99US-0132487.
Ds	1944	ATTACCACTAATGCAAGCAGCGATATAGACAAACCGAACCATCGACTACGGGGAG	2003	PR	07-MAY-1999;	99US-0132863.
Qy	388	PheLeuAlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuValAlaAla	407	PR	11-MAY-1999;	99US-0134256.
Ds	2004	TTCTAGCTGCCACATTCATCTAAACAAATCGAAGGAGATCATCTTCTAGCAGCG	2063	PR	14-MAY-1999;	99US-0134218.
Qy	408	PheSerAspPheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGlnSerAla	427	PR	14-MAY-1999;	99US-0134221.
Ds	2064	TTTTCATATTTCGACAAAGATGGAAGCGGTTTCAATACCGACGAGCTTCAACAAGCA	2123	PR	18-MAY-1999;	99US-0134370.
Qy	428	CysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIleAspLeu	447	PR	18-MAY-1999;	99US-0134768.
Ds	2124	TGTAAGAGTTCCGATAGAGGATCTTCAATGGAAGAATGATGCCGAGGTCGATCAA	2183	PR	19-MAY-1999;	99US-0134941.
Qy	448	AspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLysGlyAspGly	467	PR	21-MAY-1999;	99US-0135124.
Ds	2184	AACAATGACGGAAGCATCGACTATACGAGTTCTGTGCGATGATGCAAAAAGGAATGTA	2243	PR	24-MAY-1999;	99US-0135353.
Qy	468	ValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsnIle	482	PR	25-MAY-1999;	99US-0136021.
Ds	2244	GTGAATCTGCGAAGAAAGGCTACAAAAGT---AGCTTCAGCATT	2285	PR	27-MAY-1999;	99US-0136392.
RESULT 12				PR	28-MAY-1999;	99US-0136782.
AAC45753				PR	01-JUN-1999;	99US-0137222.
ID AAC45753 standard; DNA; 3054 BP.				PR	03-JUN-1999;	99US-0137528.
XX AAC45753;				PR	04-JUN-1999;	99US-0137502.
XX				PR	07-JUN-1999;	99US-0137724.
DT 18-OCT-2000 (first entry)				PR	08-JUN-1999;	99US-0138094.
XX				PR	10-JUN-1999;	99US-0138540.
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47639.				PR	14-JUN-1999;	99US-0138847.
XX				PR	16-JUN-1999;	99US-0139119.
KW Hybridisation assay; genetic mapping; gene expression control;				PR	16-JUN-1999;	99US-0139452.
KW protein identification; signal transduction pathway;				PR	17-JUN-1999;	99US-0139453.
KW metabolic pathway; promoter; termination sequence; ss.				PR	18-JUN-1999;	99US-0139461.
XX				PR	18-JUN-1999;	99US-0139462.
OS Arabidopsis thaliana.				PR	18-JUN-1999;	99US-0139463.
XX				PR	18-JUN-1999;	99US-0139454.
XX				PR	18-JUN-1999;	99US-0139455.
PN EP1033405-A2.				PR	18-JUN-1999;	99US-0139456.
PD 06-SEP-2000.				PR	18-JUN-1999;	99US-0139457.
XX				PR	18-JUN-1999;	99US-0139458.
XX				PR	18-JUN-1999;	99US-0139459.
XX				PR	18-JUN-1999;	99US-0139460.
XX				PR	18-JUN-1999;	99US-0139461.
XX				PR	18-JUN-1999;	99US-0139462.
XX				PR	18-JUN-1999;	99US-0139463.
XX				PR	18-JUN-1999;	99US-0139750.
XX				PR	18-JUN-1999;	99US-0139763.
XX				PR	21-JUN-1999;	99US-0139817.
XX				PR	22-JUN-1999;	99US-0139899.
XX				PR	23-JUN-1999;	99US-0140353.
XX				PR	23-JUN-1999;	99US-0140354.
XX				PR	24-JUN-1999;	99US-0140695.
XX				PR	28-JUN-1999;	99US-0140823.
XX				PR	29-JUN-1999;	99US-0140991.
XX				PR	30-JUN-1999;	99US-0141287.
XX				PR	01-JUL-1999;	99US-0141842.
XX				PR	02-JUL-1999;	99US-0142154.
XX				PR	06-JUL-1999;	99US-0142390.
XX				PR	08-JUL-1999;	99US-0142803.
XX				PR	09-JUL-1999;	99US-0142920.
XX				PR	12-JUL-1999;	99US-0142977.
XX				PR	13-JUL-1999;	99US-0143542.
XX				PR	14-JUL-1999;	99US-0143624.
XX				PR	15-JUL-1999;	99US-0144005.
XX				PR	16-JUL-1999;	99US-0144085.
XX				PR	16-JUL-1999;	99US-0144086.
XX				PR	19-JUL-1999;	99US-0144325.
XX				PR	19-JUL-1999;	99US-0144331.
XX				PR	19-JUL-1999;	99US-0144332.
XX				PR	19-JUL-1999;	99US-0144333.
XX				PR	19-JUL-1999;	99US-0144334.
XX				PR	19-JUL-1999;	99US-0144335.
XX				PR	20-JUL-1999;	99US-0144352.
XX				PR	20-JUL-1999;	99US-0144632.

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PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0147935.
PR 11-AUG-1999; 99US-0148171.
PR 12-AUG-1999; 99US-0148319.
PR 13-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150894.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155137.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.

PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Alignment Scores:
Pred. No.: 2,1e-157 Length: 3054
Score: 1703.00 Matches: 323
Percent Similarity: 78.66% Conservative: 64
Best Local Similarity: 65.65% Mismatches: 81
Query Match: 65.68% Indels: 24
DB: 21 Gaps: 2

US-09-848-806-1 (1-495) x AAC45753 (1-3054)
Qy 2 GluThrLysProAsnProArgArgPro----- 10
Db 1525 GAGACGAAAGCTGACCTCAGAGCCCTAACATATGAGGAGAGTCCAGTGCAGGCGTT 1584
Qy 11 ---SerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHisTyrLeuGly 29
Db 1585 AGAACTGAGTCAGTGTTCGAGAGGAACTGAAAACTTTAAGGAGTCTTATTATTAGG 1644
Qy 30 LysIleLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGluLysSerThrSer 49
Db 1645 AGGAACTTGGCAAGGGCAATTTGGACACCGTTTTTATGCGCTTGAGAAAGTACTGG 1704
Qy 50 AlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArgGluAspTyrGlu 69
Db 1705 AACGAATATCGTGCAGTCGATTCCAGAGAGGAGCTTTTGACTGATGAGGATGTTAA 1764
Qy 70 AspValTrpArgGluIleGlnIleMetHisHisLeuSerGluHisProAsnValValArg 89
Db 1765 GATGTGAGAAGAGAGATTTCAGATAATGTCATCACTTGGCTGGTCATCCGAATGTTATCT 1824
Qy 90 IleLysGlyThrTyrGluAspSerValPheValHisIleValMetGluValCysGluGly 109
Db 1825 ATTAAGGTGCTTATGAGGATGTTGTGCGGTACATCTCTGTGATGGAGTTGTGTGCGGT 1884
Qy 110 GlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGluAlaValLys 129
Db 1885 GCGGAGCTTTTGATAGAAATTATTCACGTGGACATTACACTGAGAGAAAGCTGCTGAG 1944
Qy 130 LeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArg 149
Db 1945 CTTGCGAGAAACCACTTGTGGGTTTATAGAGCTTGTCACTCTCTTGGTGTATGATCGG 2004
Qy 150 AspLeuLysProGluAsnPheLeuPheAspSerProLysAspAlaLysLeuLysAla 169
Db 2005 GACCTCAAGCAGAGAAATTTCTTATTGTTAGTAGAGAGAGAGATTCCCTGTTGAAACG 2064
Qy 170 ThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAspValValGly 189
Db 2065 ATCGACTTTGGACTCTCAATGTTCTTTAAGCCAGATGAGGTTTTTACAGATGTTGTGGT 2124
Qy 190 SerProTyrTyrValAlaProGluValLeuLysCysTyrGlyProGluIleAspVal 209
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Db 2125 AGTCGTAATTATGTAGTCCAGAACTTCTTAGAAGCGTTATGTCCTGAATCATCATGTG 2184
Qy 210 TrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPheTrpAla--- 228
Db 2185 TGGAGTGTGTGTGTGATTTTACATTTTGTAGCGAGTTCTCTCTTCTGGCCGCG 2244
Qy 229 -----GluThrGluSerGlyIlePheArgGln 237
Db 2245 TCTGAGTAATAATTTGTTTCCATGAATAATATACAGAAACCGAACGAGTATTTTCAGGAG 2304
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAla 257
Db 2305 GTCCTTCATGAGATCTTGACTTTTCATCTGATCCATGCGCAAGCATCTCTGAAGCGG 2364
Qy 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db 2365 AAAGACTTGGTAAGGAAATGCTTGTTCGAGACCCCAAGCGAAGACTAACCGCATCAA 2424
Qy 278 AlaLeuCysHisProTyrIleValAspGluGlnAlaProAspLysProLeuAspPro 297
Db 2425 GTATTATGTCATCCATGGTACAGATTGACGGTGTGGCTCCAGATAAACCTCTGACTCT 2484
Qy 298 AlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeu 317
Db 2485 GCTGTCTCTGAGCGGTATGAAGCAATTTCTGCAATGAACAAGTTCAAGAAAATGCTCTT 2544
Qy 318 ArgValIleAlaGluArgLeuSerGluGluGluIleGlyLeuLysGluLeuPheLys 337
Db 2545 AGAGTCATAGCTGAGAGCTTATCTGAGAGAAATAGCGGTTTAAACAAATGTTCAAG 2604
Qy 338 MetIleAspThrAspAsnSerGlyThrIlePheGluGluLeuLysAlaGlyLeuLys 357
Db 2605 ATGATAGACGACAGACAATAGTGGTCAGATCACTTTTGAAGAACTGAAGACGAGCTAAA 2664
Qy 358 ArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIle 377
Db 2665 CGAGTGTGTGCAATCTCAAGAGAGTCAGAGATTCTTGATCTTAATGCAAGCTGCTGATGT 2724
Qy 378 AspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLys 397
Db 2725 GACAAATAGCGAATAGATAGACTACAAAGATTTCATAGCCGCCCACTTCATCTAAACAAA 2784
Qy 398 MetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly 417
Db 2785 ATAGAGAGAGAGGACCAATTTGTTCGCCCTTCTCTTACTTTGACAGGACGAGGTGGC 2844
Qy 418 TyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrPro 437
Db 2845 TTTATCACCCCGGACGAGCTTCAACAAGCTTTCGGAAGAGTTTGGTGTGAAGATGCCCGC 2904
Qy 438 LeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGlu 457
Db 2905 ATAGAAGAAATGATCGCGATGTTGATCAAGCAAGGATGGCAAGATAGACTACAACGAG 2964
Qy 458 PheThrAlaMetMetArgLysGlyAspGlyValGly 469
Db 2965 TTTTGTGCAATGATGCAGAAAGGAGCATATATGGGA 3000
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## RESULT 13

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AAF74277
ID AAF74277 standard; DNA; 2334 BP.
AC AAF74277;
XX 04-MAY-2001 (first entry)
DE Rice calcium dependent protein kinase clone #1.
XX Calcium dependent protein kinase; CDPK; herbicide resistance;
KW paraquat; diquat; crop production; ds.
XX Oryza sativa.
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XX PN W0200107592-A2.
XX PD 01-FEB-2001.
XX PF 26-JUL-2000; 2000WO-GB02876.
XX PR 27-JUL-1999; 99GB-0017642.
XX PA (ZENE ) ZENECA LTD.
XX PI Holt CD, White AJ, Michael AJ, Osborn RW;
XX DR WPI; 2001-168549/17.
XX PT Producing herbicide resistance plants by inhibiting calcium dependent
PT protein kinase in plants or by providing an intracellular vacuolar
PT transporter capable of transporting agrochemical into plant vacuole
XX Claim 18; Page 39; 50pp; English.
XX The present invention describes a method of producing plants which are
XX resistant to the herbicides paraquat and diquat, involving inhibiting in
XX the plants a calcium dependent protein kinase (CDPK) and selecting those
XX plants which are resistant to the agrochemical of interest. This is
XX useful in the production of crops with herbicide resistance.
XX SQ Sequence 2334 BP; 659 A; 430 C; 625 G; 620 T; 0 other;
Alignment Scores:
Pred. No.: 4.83e-146 Length: 2334
Score: 1586.00 Matches: 304
Percent Similarity: 78.15% Conservative: 68
Best Local Similarity: 63.87% Mismatches: 102
Query Match: 61.16% Indels: 2
DB: 22 Gaps: 2
US-09-848-806-1 (1-495) x AAF74277 (1-2334)
Qy 11 SerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHisTyrLeuLeuGlyLys 30
Db 537 TCTATCAATGTCTTGGCGGAGACACAGCGACCTTAAGGAGCATATATCATCTGTCGG 596
Qy 31 LysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGluLysSerThrSerAla 50
Db 597 AAGCTTGTGTCAGGCCCTAGTTGGCACAACTTACCTCTGTACCGAGATCAATACAGGGTGT 656
Qy 51 AsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArgGluAspTyrGluAsp 70
Db 657 GAGTATGCTTGCAGAGACCATCCCAAGCGCAAGCTCATCAACAGGAGGATGTAGAAGAT 716
Qy 71 ValTrpArgGluIleGlnIleMetHisLeuSerGluHisProAsnValValArgIle 90
Db 717 GTGCGCGGTGAGATTTCAGATAATGCACCATTTGTTCGGGCCCAAGAAATGTTGTTGCAATC 776
Qy 91 LysGlyThrTyrGluAspSerValPheValHisIleValMetGluValCysGluGly 110
Db 777 AAGGATGCTATGAGGATGGCAAGCGGTGCACATTGTGATGGAGCTCTGCGCTGTGGG 836
Qy 111 GluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLeu 130
Db 837 GAGCTCTTTCAGAGATTTCAGGAGAGGGCATTTACAGCGAGCGGAGGCTGCAGAGCTT 896
Qy 131 IleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAsp 150
Db 897 ATAAGATAAATTTGTACGATTGTGGCTATGTGCCATTTCGCTCGGGGTGATGCACCGTAT 956
Qy 151 LeuLysProGluAsnPheLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThr 170
Db 957 CTTAAGCCAGAAAATTTCTCTCTTTTGGATAAAGATGATGATCTGTCAATAAGGCAATA 1016
Qy 171 AspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySer 190
|||||
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Db 1017 GATTTGGCTATCCGTTGTTCTTCAAAACAGGTCAGGTTTTCAGTGAAGTGGTGGAGT 1076  
QY 191 ProTyrTyrValalaProGluValLeuLeuLysCysTyrGlyProGluIleAspValTrrp 210  
Db 1077 CCATATTATGTTCTCTAGGTTATTCACAAACGTTATGACCAAGTCTGATGTTGG 1136  
QY 211 SerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPheTrrpAlaGluThr 230  
Db 1137 TCAGCTGGAGTGATATCTTACGTTTGTCTGAGTGGAGTGCACCATTTTGGGAGAGACA 1196  
QY 231 GluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTrrp 250  
Db 1197 CAACAAGGATATTTGATGAGTCTCTGAAGGTCACATTTTCAATCTGATCCATGG 1256  
QY 251 ProThrIleSerGluAlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLys 270  
Db 1257 CCAAGATATCTGACAGTGCNAAGGATCTTATAAGAAAAATGCTCTCTCATTTGCCCTTCG 1316  
QY 271 LysArgIleSerAlaHisGluAlaLeuCysHisProTrrpIleValAspGluGlnAlaAla 290  
Db 1317 GAGCGTTTGAAGCCCATGAAGTGTCTAAGGCATCTCTTGGATCTGTGAAAAATGGAGTTGCC 1376  
QY 291 ProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsn 310  
Db 1377 ACTGATCAAGCTCTGGATCCAGTGTATCTCTCGGCTCAAACAATCTCTGCAATGAAC 1436  
QY 311 LysIleLysLysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluIleGly 330  
Db 1437 AAGTTAAAGAAAGTGGCTCTGAGAGTGATAGCTGAGCGTCTTTTCAGAGGAGGAGATTGCT 1496  
QY 331 GlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGlu 350  
Db 1497 GGGTTAAGGAAATGTTTCAAGCGCAGTGGACACAAAAATAGAGGTGTAAATCACTTTCCGT 1556  
QY 351 GluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSer 370  
Db 1557 GAGCTTAGAGAAAGTTTAAAGAGATTTGGCGTGAATTTAAGGATACAGAGATTGGTAT 1616  
QY 371 LeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAla 390  
Db 1617 ATAATGGAAGCGGCACACACGACAATAATGTAAACAATCCATTTATGAAGAAATTTATTGCT 1676  
QY 391 AlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAsp 410  
Db 1677 GCNACTCTACCTTTAACAGATAGAACGTTGAGAGCACCTCTGTCGAGCTTTTACATAT 1736  
QY 411 PheAspLysAspGlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGlu 430  
Db 1737 TTTGACAAAGATGGGAGTGGTTATATACAGTTTGACAAGCTTCAACAGCTTGTGGAGAA 1796  
QY 431 PheGlyLeuCysAspThrProLeuAspAspMetIleLysGluIleAspLeuAspAsnAsp 450  
Db 1797 CATAACATGGAGGATTCACCTCTGAAGAGATTATTTTCAGAGGTTGATCAAAACAATGAC 1856  
QY 451 GlyLysIleAspSerGluPheThrAlaMetMetArgLysGlyAspGlyValGlyArg 470  
Db 1857 GGCCAAATTTGATCCCGCAATTTTGGCCATGATG---CAAGGCAACGACCTTGGACTA 1913  
QY 471 Ser---ArgThrMetMetLysAsnLeuAsnPheAsnIleAlaAspAla 485  
Db 1914 GGGTGGCAACAATGGAAGCAGTTTGAATGTAGCATTAAAGACGCCA 1961

## RESULT 14

AAF74281

ID AAF74281 standard; DNA; 1647 BP.

XX

AC AAF74281;

XX

DT 04-MAY-2001 (first entry)

XX

DE Liverwort calcium dependent protein kinase clone #1.

XX

KW Calcium dependent protein kinase; CDPK; herbicide resistance;

KW paraquat; diquat; crop production; ds.  
XX Marchantia polymorpha.  
XX WO200107592-A2.  
XX  
PD 01-FEB-2001.  
XX  
XX 26-JUL-2000; 2000WO-GB02876.  
XX  
XX 27-JUL-1999; 99GB-0017642.  
XX  
XX (ZENE ) ZENECA LTD.  
XX  
XX Holt CD, White AJ, Michael AJ, Osborn RW;  
XX WPI; 2001-168549/17.  
XX  
XX Producing herbicide resistance plants by inhibiting calcium dependent  
XX protein kinase in plants or by providing an intracellular vacuolar  
XX transporter capable of transporting agrochemical into plant vacuole  
XX  
XX Claim 18; Page 42; 50pp; English.

CC The present invention describes a method of producing plants which are  
CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
CC plants which are resistant to the agrochemical of interest. This is  
CC useful in the production of crops with herbicide resistance.

XX Sequence 1647 BP; 447 A; 349 C; 465 G; 386 T; 0 other;

## Alignment Scores:

Pred. No.: 7 01e-141 Length: 1647  
Score: 1531.50 Matches: 294  
Percent Similarity: 76.72% Conservative: 75  
Best Local Similarity: 61.12% Mismatches: 105  
Query Match: 59.06% Indels: 7  
DB: 22 Gaps: 3

US-09-848-806-1 (1-495) x AAF74281 (1-1647)

QY 1 MetGluThrLysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrPro 20  
Db 169 ATCTCTGCCAAACAAAGCCACGTTGACTGGCAAT---GTGCTCGCAGCCACTGAA 225  
QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThr 40  
Db 226 GATGTCGATGCCATTTTACACCTCGGACGGAACTGGTGTGTCAGTTGGTGTGTCAGC 285  
QY 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60  
Db 286 CATTTGTGTACGCACCAAGGTTACAGGTGAGCTTTTAGCTTGAAGTCAATTTGCGAAGAGG 345  
QY 61 LysLeuValCysArgGluAspTyrGluAspValTrrpArgGluIleGlnIleMetHisHis 80  
Db 346 AAGTTGACCAATAAGGATGACGTAGAGGATGTTTCGAGGGGAAGTGCAGATCATGCACCAC 405  
QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100  
Db 406 TTAGAGGGGCAGAGAACAATTTGCGAAATTTGAAGGGGGCCCTATGAGGATAAACCAACGTG 465  
QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120  
Db 466 CATCTCGTCATGAGCTTTGCTGCGGAGAACTCTTCGACCGCAATTTATTCAGCGGGGC 525  
QY 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140  
Db 526 CACTACAGTGAGAGGCTCTGTCAGCTCTATGTAGAACTATAGTCAAGTGGTTCAGACG 585  
QY 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160  
Db 586 TGCCATTCTCGGGAGTTATGCACCGGGATCTGAAGCCCGGAAATTTTCTGCTTGTCTAAC 645

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QY 161 ProLysAspAlaIleLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrIlePro 180
DB 646 AAGAGGAGGAGTGCACCCCTGAAGGAGGAGGATTTGGTCTTCTCTTCAAGCT 705
QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
DB 706 GGAGAGGTTTACAGATATCGTTGGAAGTCTTACTACGTGGCAGCAGAGGTTTGGT 765
QY 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeu 220
DB 766 CGTAACATATGGCCAGAGGCTGATGTTGGAGTCCCGAGTCATTTCTTACATCTTTTG 825
QY 221 SerGlyValProProPheThrAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
DB 826 TCGGAGTCCCTCTCTTCTGGCAGAACCCAGGATATTTTGTGCGGCTAATGCAC 885
QY 241 GlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeu 260
DB 886 GGTCAATATGATTTCACTAGTATCTTGGCCTTCAATTTCTCAAAAGCGCAAGATCTG 945
QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLysCys 280
DB 946 GTAAAGAGGATGCTCAACAGAACCCAAAGAGGAGGATTTGACGGCCCATGAATTTAAGT 1005
QY 281 HisProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300
DB 1006 CACCATGATTTAGTTGTCGGAGAGCCACAGACAAACACCTTGACACCGCGTGTG 1065
QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysMetAlaLeuArgValIle 320
DB 1066 TCTAGATTTGAAGCAATTCACCGCTATGAACAAAGCTCAAGAACTTGCTCTGAAGTTATC 1125
QY 321 AlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
DB 1126 GCAGAGTCTCTCTGAAGAGAGATCATGGGATTTGAAGGAGATTTTAAAGATGATGAC 1185
QY 341 ThrAspAsnSerGlyThrIleThrPheGluLeuLysAlaGlyLeuLysArgValGly 360
DB 1186 ACACACAACAGTGTGTACAACTCACGTCGAGGAGTTGAAGGATGCTCTCAAAAGCAGGA 1245
QY 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
DB 1246 TCAAACTGCGAGAGTCAGAGTCCGCGAGCTAATGCGAGCTGCTGATGTGATGGAAT 1305
QY 381 GlyThrIleAspTyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArg 400
DB 1306 GGCACTATTGACTACTTGGAGTTTCATACGGCAACCATGCACTTGAATAAGATAGAAG 1365
QY 401 GluGluLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
DB 1366 GAAGATCATCTTTACGCTGCTTTTCAGCATTTTTCAGGACAGCAGCTGGGTTTCATCACC 1425
QY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp---ThrProLeuAsp 439
DB 1426 ATGAAGAGCTTTGAACAGGCTTTAATTAAGCAGCGGATGGAGATCTGATCTCTGAAA 1485
QY 440 AspMetIleLysGluIleAspLeuAspAspGlyLysIleAspPheSerGluPheThr 459
DB 1486 GAAATTTATAGGAGGTTGACACTGATCATGATGACGCAATCACTACGACGAGTTCGTT 1545
QY 460 AlaMetMetArgLysGly-----AspGlyValGlyArgSerArgThrMet 474
DB 1546 GCCATGATGCTAAAGGTACCCCTGGACACCAAGAGGCGCACAGGAGGATATAAGTAAT 1605
QY 475 Met 475
DB 1606 ATG 1608
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RESULT 15  
AAF74282  
ID AAF74282 standard; DNA; 1647 BP.  
XX

```
AC AAF74282;  
DT 04-MAY-2001 (first entry)  
DE Liverwort calcium dependent protein kinase clone #2.  
KW Calcium dependent protein kinase; CDPK; herbicide resistance;  
KW paraquat; diquat; crop production; ds.  
OS Marchantia polymorpha.  
PN WO200107592-A2.  
XX  
PD 01-FEB-2001.  
XX  
PP 26-JUL-2000; 2000WO-GB02876.  
XX  
PR 27-JUL-1999; 99GB-0017642.  
XX  
PA (ZENE ) ZENECA LTD.  
PI Holt CD, White AJ, Michael AJ, Osborn RW;  
XX WPI; 2001-168549/17.  
XX  
PT Producing herbicide resistance plants by inhibiting calcium dependent  
PT protein kinase in plants or by providing an intracellular vacuolar  
PT transporter capable of transporting agrochemical into plant vacuole  
PS Claim 18; Page 42; 50pp; English.  
XX  
CC The present invention describes a method of producing plants which are  
CC resistant to the herbicides paraquat and diquat, involving inhibiting in  
CC the plants a calcium dependent protein kinase (CDPK) and selecting those  
CC plants which are resistant to the agrochemical of interest. This is  
CC useful in the production of crops with herbicide resistance.  
XX  
SQ Sequence 1647 BP; 445 A; 348 C; 464 G; 390 T; 0 other;
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Pred. No.: 3,43e-140 Length: 1647  
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DB: 22 Gaps: 3
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QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrThr 40  
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QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHis 80  
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QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100  
DB 406 TTAGAGGGGCAGAGAACAATGTCGAATTCAGAGGGGCCCTATGAGGATAACACACAGCTG 465  
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Search completed: November 28, 2003, 10:56:57  
Job time : 473 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:43:12 ; Search time 3093 Seconds  
(without alignments)  
3889.659 Million cell updates/sec

Title: US-09-848-806-1  
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Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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12: gb\_est3:\*  
13: gb\_est4:\*  
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24: em\_gss\_pro:\*  
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28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	1557	60.0	2566	11	AY109374	AY109374 Zea mays
3	1460	56.3	2298	11	AY109401	AY109401 Zea mays
C						
4	1362.5	52.5	1628	11	AY109463	AY109463 Zea mays
5	1125	43.4	835	10	BG647837	BG647837 EST509456
6	1123	43.3	814	12	BG878737	BG878737 EST513724
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7	1088.5	42.0	882	29	CG331661	CG331661 OGIAY83TV
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9	1011	39.0	697	12	BJ302783	BJ302783 BJJ02783
10	996	38.4	777	13	BQ990683	BQ990683 QGF20N08
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12	979	37.8	686	12	B1178776	B1178776 EST519721
13	961	37.1	751	13	BQ865474	BQ865474 QCSA16.Y
14	958	36.9	827	14	CB677374	CB677374 OSJNEP14E
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28	902	34.8	747	13	BQ970309	BQ970309 QHB41K23
29	900	34.7	635	9	AW587489	AW587489 IPRGH2007
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# ALIGNMENTS

RESULT 1

AY109473

LOCUS

DEFINITION

AY109473

ACCESSION

AY109473.1

VERSION

KEYWORDS

SOURCE

ORGANISM

Zeae mays

Zeae mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

1 (bases 1 to 2380)

AY109473 Zea mays 2380 bp mRNA linear HTC 17-OCT-2002

AY109473.1 GI:21213206

**AUTHORS** Hayney,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
**TITLE** Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes  
**JOURNAL** Unpublished (2002)  
**REFERENCE** 2 (bases 1 to 2380)  
**AUTHORS** Coe,E.H.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA  
**COMMENT** If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.

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Alignment Scores:  
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 Score: 1560.00 Matches: 303  
 Percent Similarity: 76.30% Conservative: 48  
 Best Local Similarity: 65.87% Mismatches: 107  
 Query Match: 60.16% Indels: 2  
 DB: 11 Gaps: 2

US-09-848-806-1 (1-495) x AY109473 (1-2380)

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 2566)  
AUTHORS Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,  
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.  
TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of  
Overgo Probes  
JOURNAL Unpublished (2002)  
REFERENCE 2 (bases 1 to 2566)  
AUTHORS Coe,E.H.  
TITLE Direct Submission  
JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
Missouri, Columbia, MO 65211 USA  
COMMENT If you are interested in getting corresponding physical clones,  
these are publicly available from ZmDB and may be found by BLAST  
searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
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www.zmdb.iastate.edu.

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contigs to seed DuPont contigs, this resource was  
assembled by DuPont as part of a collaboration for the  
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Mapping Project"

BASE COUNT 440 a 680 c 777 g 420 t 249 others  
ORIGIN

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Percent Similarity: 75.46% Mismatch: 69  
Best Local Similarity: 61.35% Indels: 114  
Query Match: 60.05% Gaps: 7  
DB: 11

US-09-848-806-1 (1-495) x AY109374 (1-2566)

QY 5 ProAsnProArgArgProSerAsn-----ThrValLeuProTyrGln 18  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 688 CCGCAGGTGAAGCGCTGTTCGAGCCGCCGGCTGCTGCTGGGGTGCGTGCAGGCCAAG 747  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
QY 19 ThrProArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnPheGly 38  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 748 ACGGAGAACCTCAAGAGCAAGTAGCTACNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTTCCGC 807  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
QY 39 ThrThrTyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIlePro 58  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 808 ACACGCGACCTGTCGCTGGAGCGCGCACCGGGAAGGAGCTCGCGTGCAGTCATCATCTG 867  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
QY 59 LysArgLysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMet 78  
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Db 868 AACGCGAAGCTGGCGACGACGACGAGCTGGAGAGCTGCGCGCGGAGATCCAGATAATG 927  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
QY 79 HisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerVal 98  
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Db 928 CACCACCTGGCGGCCACCCCAGCGTGGTCCGATCCGCGGCCGCTACGAGGACGCCGCTG 987  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
QY 99 PheValHisIleValMetGluValCysGluGlyGlyLeuPheAspArgIleValSer 118  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
Db 988 GCCGTGCACCTCGCTCATGGAGCTCTCGCGCGCGCGGAGCTGTTCACCGGATCGTGGCG 1047  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
QY 119 LysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValVal 138  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :  
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :

RESULT 3	AV109401	2298 bp	mRNA	linear	HTC 17-OCT-2002
LOCUS	AV109401	2298 bp	mRNA	linear	HTC 17-OCT-2002
DEFINITION	Zea mays	2298 bp	mRNA	linear	HTC 17-OCT-2002
ACCESSION	AV109401	2298 bp	mRNA	linear	HTC 17-OCT-2002
VERSION	AV109401.1	2298 bp	mRNA	linear	HTC 17-OCT-2002
KEYWORDS	HTC	2298 bp	mRNA	linear	HTC 17-OCT-2002
SOURCE	Zea mays	2298 bp	mRNA	linear	HTC 17-OCT-2002
ORGANISM	Zea mays	2298 bp	mRNA	linear	HTC 17-OCT-2002
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	2298 bp	mRNA	linear	HTC 17-OCT-2002
AUTHORS	1 (bases 1 to 2298)	2298 bp	mRNA	linear	HTC 17-OCT-2002
TITLE	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.	2298 bp	mRNA	linear	HTC 17-OCT-2002
JOURNAL	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes	2298 bp	mRNA	linear	HTC 17-OCT-2002
AUTHORS	Unpublished (2002)	2298 bp	mRNA	linear	HTC 17-OCT-2002
TITLE	2 (bases 1 to 2298)	2298 bp	mRNA	linear	HTC 17-OCT-2002
JOURNAL	Coe, E.H.	2298 bp	mRNA	linear	HTC 17-OCT-2002
AUTHORS	Direct Submission	2298 bp	mRNA	linear	HTC 17-OCT-2002
TITLE	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA	2298 bp	mRNA	linear	HTC 17-OCT-2002
JOURNAL	These are publicly available from ZmDB and may be found by BLAST searching at MSU, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.	2298 bp	mRNA	linear	HTC 17-OCT-2002
COMMENT	Location/Qualifiers	2298 bp	mRNA	linear	HTC 17-OCT-2002
FEATURES	1..2298	2298 bp	mRNA	linear	HTC 17-OCT-2002
source	/organism="Zea mays"	2298 bp	mRNA	linear	HTC 17-OCT-2002
	/mol_type="mRNA"	2298 bp	mRNA	linear	HTC 17-OCT-2002
	/db_xref="MaizeDB:630430"	2298 bp	mRNA	linear	HTC 17-OCT-2002
	/db_xref="taxon:4577"	2298 bp	mRNA	linear	HTC 17-OCT-2002
	/clone_lib="Maize Mapping Project/DuPont Cornsensus Library"	2298 bp	mRNA	linear	HTC 17-OCT-2002
	/notes="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"	2298 bp	mRNA	linear	HTC 17-OCT-2002
BASE COUNT	544 a 464 c 597 g 524 t 169 others	2298 bp	mRNA	linear	HTC 17-OCT-2002
ORIGIN		2298 bp	mRNA	linear	HTC 17-OCT-2002
Alignment Scores:		2298			
Pred. No.:	9,7e-156	2298			
Score:	1460.00	278			
Percent Similarity:	76.46%	76			
Best Local Similarity:	60.04%	107			
Query Match:	56.31%	2			
DB:	11	2			
US-09-848-806-1 (1-495) x AV109401 (1-2298)					
QY	5 ProAsnProArgArgPro---SerAsnThrValLeuProTyrGlnThrProArgLeuArg 23				
Db	600 CCTGTGCGCCGACAGCCACGCGCGGACACGATTCTTGGCAAGCAGTACGAGGACGTGCGC 659				
QY	24 AspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCys 43				
Db	660 TCTGTCTACTCCCTCGGGAAGGAGCTTGGCCGGGGCCAGTTCGGGTGACATACCTCTGC 719				
QY	44 ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal 63				
Db	720 ACAGAGTTTCCTTCGGAGGAGTACGCGCTGCAAGTCCATCTCCAAGCGCAAGTCGCC 779				
QY	64 CysArgGluAspTyrGluAspValTPrArgLuuIcInIleMethHisLeuSerGlu 83				
Db	780 AGCAAGGACAGCAGGAGGACATTCGAAGGGAGATCCAGATCATGAGCACTGTCTGGG 839				

Qy 443 LysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMet 462  
 Db 1920 TCAGAGTTGACACAGATAATGAGGAGGATTAACATATGAGGAGTTTGTGCAATGATG 1979  
 Qy 463 ArgLysGly 465  
 Db 1980 AGAGGAGG 1988

RESULT 4  
 AY109463/c 1628 bp mRNA linear HTC 17-OCT-2002  
 LOCUS  
 DEFINITION Zea mays CL10776\_2 mRNA sequence.  
 ACCESSION AY109463  
 VERSION AY109463.1 GI:21213192  
 KEYWORDS HTC.  
 SOURCE Zea mays

ORGANISM  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 AUTHORS Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S.,  
 Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.  
 TITLE Maize Mapping Project/DuPont Consensus Sequences for Design of  
 Overgo Probes

JOURNAL Unpublished (2002)  
 AUTHORS 2 (bases 1 to 1628)  
 TITLE Direct Submission  
 JOURNAL Submitted (25-APR-2002) Maize Mapping Project, University of  
 Missouri, Columbia, MO 65211, USA  
 COMMENT If you are interested in getting corresponding physical clones,  
 these are publicly available from ZmDB and may be found by BLAST  
 searching at MSU, maizeap.org; ZmDB, www.zmdb.iastate.edu; TIGR,  
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the  
 maize cDNA sequences is either Virginia Walbot, Stanford or Pat  
 Schnable, Iowa State, then clones may be requested from ZmDB:  
 www.zmdb.iastate.edu.

FEATURES  
 source  
 1..1628  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /db\_xref="MaizeDB:629956"  
 /db\_xref="taxon:4577"  
 /clone\_lib="Maize Mapping Project/DuPont Consensus  
 Library"  
 /notes="this sequence is part of a project of EST  
 assemblies resulting from the application of public  
 contigs to seed DuPont contigs; this resource was  
 assembled by DuPont as part of a collaboration for the  
 overgo addressing of BACs in conjunction with the Maize  
 Mapping Project."

BASE COUNT 393 a 408 c 350 g 424 t 53 others

ORIGIN

Alignment Scores:  
 Pred. No.: 8,59e-145 Length: 1628  
 Score: 1362.50 Matches: 251  
 Percent Similarity: 76.28% Conservative: 77  
 Best Local Similarity: 58.37% Mismatches: 101  
 Query Match: 52.55% Indels: 1  
 DB: 11 Gaps: 1

US-09-848-806-1 (1-495) x AY109463 (1-1628)

Qy 35 GlyGlnPheGlyThrThrTyrLeuCysThrGluLysSerThrSerAlaSerTyrAlaCys 54  
 Db 1615 GGCCAGTCGGGTACCTACCTCGTCAGCACTCGGAGCCGGGCGGCTTCGGCTGC 1556  
 Qy 55 LysSerIleProLysArgLysLeuValCysArgGluAspTyrGluAspValTrpArgGlu 74  
 Db 1555 AAGTCCATCCGACGCGGAGGCTCGTCCACCGCGAGCATGAGGACGTCGCGCGGAG 1496

Qy 75 IleGlnIleMetHisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyr 94  
 Db 1495 GTGCAGATCATGCACCACTCACGGGCCCGNNNNNCGTCGAGCTCCGGGGAGCATAC 1436  
 Qy 95 GluAspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAsp 114  
 Db 1435 GAGACAGGCACCTCGGTCAACCTTGTTATGGAGCTTCGCGAGGCGGGAGCTCTTCGAC 1376  
 Qy 115 ArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIle 134  
 Db 1375 CGCATCATGCCAAGGCGCACTACCGACGCGNNNNNNNNNNNNNNNNNNNNNNNGATC 1316  
 Qy 135 LeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGlu 154  
 Db 1315 GTCGCCGTGTCACACAGCTGCCACTCCATNNNNNTCTTCATCGGATCTCAAGCCCGAG 1256  
 Qy 155 AsnPheIlePheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeu 174  
 Db 1255 AACTTCCTGTCTCTCAATAACAAGGAGGACTCCCGCTCAAGGCCACGACTTCGGTCTC 1196  
 Qy 175 SerValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrVal 194  
 Db 1195 TCGGTCTTCTCAAGCACGGGAGAGCTTTAAGGATCTTGTGGAGTGCATATTATGTT 1136  
 Qy 195 AlaProGluValLeuLysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyVal 214  
 Db 1135 GCTCTGAGGTACTGAAACGGAATATGGGCGAGAGGCTGACATATGGAGTCTGGGGTC 1076  
 Qy 215 IleLeuTyrIleLeuLeuSerGlyValProPheTrpIleGluThrGluSerGlyIle 234  
 Db 1075 ATTCTTTACNNNNNNNNNNCTGGTGTCTCTCTTCTGGGAGAGATGAGGATGGCATA 1016  
 Qy 235 PheArgGlnIleLeuGlnLysLeuAspPheLysSerAspProTrpProThrIleSer 254  
 Db 1015 TTTGATGCTGCTTGGCGGTCACATCGATTTCTTCTGACCTTGGCCCTTCAATATCC 956  
 Qy 255 GluAlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSer 274  
 Db 955 AATGGTGCAAGGATTTGGTTAAGAAGATGCTCGCACAGACCCCAAGAACCCCTGACT 896  
 Qy 275 AlaHisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaAlaProAspLysPro 294  
 Db 895 GCTGCTGAAATTTTGAACCAACCCATGATGATGAGAGGAGGAGGAGGAGGAGGAGGAG 836  
 Qy 295 LeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLys 314  
 Db 835 CTTGACATTACTGTCAATGTTAGAAACAGTTTCAAGGCAATGAACAGCTCAAGAAA 776  
 Qy 315 MetAlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGlu 334  
 Db 775 GTTGCAATTGAAGGTTGCTGCTGAGAACTTATCAGATGAAGAGATTATGGCCCTAAAGAA 716  
 Qy 335 LeuPheLysMetIleAspThrAspSerGlyThrIleThrPheGluGluLeuLysAla 354  
 Db 715 ATGTTTCAGATCCCTGGATACAGTACAGTGGGACAAATTAATCTTTGAAGAGCTTAAGATCT 656  
 Qy 355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla 374  
 Db 655 GGTTTACCAAACTTGGTACTAAATTTCTGAATCAGAAATTAACAAATTTGATGGAGCG 596  
 Qy 375 AlaAspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHis 394  
 Db 595 GCTGATGTTGATGGAATGGTACCATTGATTATGCGGAGTTTATATACCCCAATGCAAT 536  
 Qy 395 MetAsnLysMetGluArgGluLeuValAlaAlaPheSerAspPheAspLysAsp 414  
 Db 535 TTGAATAGATTGGAGAGGAGAGACCATCTACTCAAAAGCTTTTGAATATTTTCGATAAGGAT 476  
 Qy 415 GlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeu--- 433  
 Db 475 CACACGGATACATAACCGTAGATGAGTTGGAAGAGAGCTTTTGAAGAAAGTATGATGGA 416  
 Qy 434 CysAspThrProLeuAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIle 453

Db 415 GATGCAAAACATATAAAAGAAATCATCTGCTGAAGTAGATACAGATCATGATGGAAGATT 356  
Qy 454 AspPheSerGluPheThrAlaMetMetArg 463  
Db 355 AATTACCAAGGATTGTTGCCATGATGAGG 326

RESULT 5  
BG647837  
LOCUS  
DEFINITION  
EST509456 HOGA Medicago truncatula cDNA clone phOGA-18E5 5' end,  
mRNA sequence.  
ACCESSION  
BG647837  
VERSION  
BG647837.1 GI:13782949  
KEYWORDS  
Medicago truncatula (barrel medic)  
SOURCE  
Medicago truncatula  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids  
; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;  
Medicago.

REFERENCE  
1 (bases 1 to 835)  
Hahn M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S.,  
Utterback, T., Cho, J., and Fraser, C.M.  
ESTs from roots of Medicago truncatula treated with  
oligogalacturonides of DP 6-20  
Unpublished  
Contact: Michael G. Hahn  
Complex Carbohydrate Research Center  
University of Georgia  
220 Riverbend Road, Athens, GA 30602-4712, USA  
Tel: 706-542-4457  
Fax: 706-542-4412  
Email: hahn@crc.uga.edu  
G391443e TIGR sequence name: MTMCE27TK More information is  
available at: www.medicago.org  
Seq primer: SKmod (CTA GAA CTA gtc gat CC).

FEATURES  
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/organism="Medicago truncatula"  
/mol\_type="mRNA"  
/cultivar="A17"  
/db\_xref="taxon:3880"  
/clone="phOGA-18E5"  
/tissue\_type="3 day old seedling roots"  
/dev\_stage="24 hours after treatment in the dark at 26 C  
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the  
presence of 100 ug/ml Gentamicin"  
/lab\_host="XLOLR"  
/clone\_lib="HOGA"  
/note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA  
was directionally ligated into the Unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-Zap phage using Ex-aseist  
helper phage and propagated in SOLR cells."

BASE COUNT 230 a 137 c 210 g 258 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 5,17e-118 Length: 835  
Score: 1125.00 Matches: 223  
Percent Similarity: 87.77% Conservative: 21  
Best Local Similarity: 80.22% Mismatches: 34  
Query Match: 43.39% Indels: 2  
DB: 10 Gaps: 0

US-09-848-806-1 (1-495) x BG647837 (1-835)  
Qy 114 AspArgIleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThr 133  
Db 2 GATATGATTGTGCAGAAAGGGCATTATAGTGAGAGACAAGCTGCTAAGTTGATTAGAACT 61

Qy 134 IleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysPro 153  
Db 62 ATTGTTGAGGTTGTTGAAGCTTGTCATTTCTTGGATTATGCACAGAGACCTTAACCT 121  
Qy 154 GluAsnPheLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThrAspPheGly 173  
Db 122 GAGAAATTTTGTGTTGATTCTGTTGATGAAGATGCTCTCTCAAAACTATTGATTTGGT 181  
Qy 174 LeuSerValPheThrLysProGlyGlnThrLeuThrAspValValGlySerProThrTyr 193  
Db 182 TTGCTGTGTTTTTCAAGCCAGGTGAATCTTTAGTGATGTTGTTGGAAGCCCACTAT 241  
Qy 194 ValAlaProGluValLeuLysLysCysThrGlyProGluIleAspValThrSerAlaGly 213  
Db 242 GTTGGCCAGAGGCTTGTGCACAAACATATGACCTGTAAGCAGACGTTGGAGTGCTGT 301  
Qy 214 VallLeuThrIleLeuLeuSerGlyValProProPheThrAlaGluThrGluSerGly 233  
Db 302 GTTATTTTGTACATCTTATTAAAGCGGGTCTCCGTTTTCGGCCGAGACCCATCAAGG 361  
Qy 234 IlePheArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProThrProThrIle 253  
Db 362 ATCTTCAGACAGATTTTCCAAGGAAACTTTGATTTCCGGTCTGAGCCGTGGCGATT 421  
Qy 254 SerGluAlaLysAspLeuIleThrLysMetLeuGluArgSerProLysLysArgIle 273  
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Qy 274 SerAlaHisGluAlaLeuCysHisProThrIleValAspGluGlnAlaAalaProAspLys 293  
Db 482 ACAGCTCACCAAGTGCTCTGTCAACCCGTGGATTTCGATGATAACATTCACACAGATAA 541  
Qy 294 ProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLys 313  
Db 542 CCTCTTGATTCTGCTGTTTTATCTCGCTCGAAGCAGTTCTCTGCGATGAATAAACTTAA 601  
Qy 314 LysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyGlyLeuLys 333  
Db 602 AAGATGCTTTACGTGTTATTCGGAGAGGCTTCTCAGGAGAAATTTGGTTGGTTGAAG 661  
Qy 334 GluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLys 353  
Db 662 GAGTTATTCAGGATGCTGATGCTGTAATAGTGAACACTATACTTGGGAGAGTTAA 721  
Qy 354 AlaGlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAsp 373  
Db 722 GAAGGCTTAAAGCGAGTAGGATCTGAACCTTATGGAGTCTGAATC-AAAGGATCTTTATG 780  
Qy 374 AlaAlaAspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAala 391  
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RESULT 6  
BG887873  
LOCUS  
DEFINITION  
EST513724 cSTD Solanum tuberosum cDNA clone cSTD7P13 5' sequence,  
mRNA sequence.  
ACCESSION  
BG887873  
VERSION  
BG887873.1 GI:14264959  
KEYWORDS  
Solanum tuberosum (potato)  
ORGANISM  
Solanum tuberosum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.  
REFERENCE  
1 (bases 1 to 814)  
van der Hoeven, R., Bezzerides, J., Ewing, E., Cho, J., Chlemingo, A.,  
Bougr, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.  
Generations of ESTs from dormant potato tubers  
Unpublished  
Contact: Robin Buell  
The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

This clone can be obtained from the University of Arizona Genomics Institute. Orders can be made through URL:

http://genome.arizona.edu/orders/

Seq primer: M13F-R.

# FEATURES

Location/Qualifiers

1..814  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="CSD7P13"  
/tissue\_type="dormant tuber"  
/dev\_stage="one month post-harvest"  
/lab\_host="SOLR"  
/clone\_lib="cSTD"  
/note="Vector: pBluescript SK(-); Site\_1: EcoRI; Site\_2: XhoI; This library targets genes expressed in dormant tubers. This library was made from sections of dormant tuber, avoiding the buds and epidermis. Tubers were stored for one month post-harvest at 4°C. The tuber was peeled, well away from the surface. Then it was chopped into 1-2 mm cubes and immediately frozen in liquid nitrogen. This library is noted as P4 in Tanksley lab notebooks."

242 a 146 c 191 g 235 t  
BASE COUNT  
ORIGIN

Alignment Scores:  
Pred. No.: 8 43e-118 Length: 814  
Score: 1123.00 Matches: 215  
Percent Similarity: 90.0% Conservative: 30  
Best Local Similarity: 79.04% Mismatches: 26  
Query Match: 43.31% Indels: 2  
DB: 12 Gaps: 0

US-09-848-806-1 (1-495) x BG887873 (1-814)

QY 125 ArgGluAlaValLysLeuLeuLysThrLeuLeuGlyValValGluAlaCysHisSerLeu 144  
DB 2 AGAAAAGCTGCACAAATTGATGAACACTATTGTCAAAGTTGTGGAGGCTTGCTATCTCT 61  
QY 145 GlyValMetHisArgAspLeuLysProGluAunPheLeuPheAspSerProLysAspAsp 164  
DB 62 GGGGTATGTCATAGAGATCTCAACCTGAGAAATTTCTTTTGTAGCTCTGATGAAGAT 121  
QY 165 AlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeu 184  
DB 122 GCTAAGCTTAAGCTACTGATTTTGGTCTCTATTTCTATAGCCAGGCGAGTATTTC 181  
QY 185 TyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGly 204  
DB 182 TCAGATGTTGTGAAGTCCATATTATGTTGCTCCTGAAGTGTGCACAAATACTATGGG 241  
QY 205 ProGluLeuAspValTyrSerAlaGlyValLleLeuTyrLleLeuLeuSerGlyValPro 224  
DB 242 CCTGAATAGAGCTGTGGAGTCTGGAGTCATCCCTTTATATCTTGTATGTGGGTTCTCT 301  
QY 225 ProPheTyrAlaGluThrGluSerGlyLlePheArgGlnLeuGluGlnLysLeuAsp 244  
DB 302 CTTTCTGGCTGACACAGACAACTGGTATCTTCAACAGATATTAAAGGAAGATAGAC 361  
QY 245 PheLysSerAspProTyrProThrLysSerGluAlaAlaLysAspLeuLleTyrLysMet 264  
DB 362 TTTGAATCAGAACCTTGGCCTCAGATTCTGTAGTAGTGCAAAAGATTGGTAAAGAAGATG 421  
QY 265 LeuGluArgSerProLysLysArgLleSerAlaHisGluAlaLeuCysHisProTrpLe 284  
DB 422 CTACACGGGATCTTACAGACAGATTAACCGGCATCAAGTCTATGTCATCTCTGGATT 481  
QY 285 ValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLys 304  
DB 482 GTGGATGATAATGTTGCTCCAGACAGGCCCTTGGTCTGTCAGTTTGTCCGCCCTAAAG 541

QY 305 GlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLeu 324  
DB 542 CAGTTCTATGATATGAACAACTTAAAGAGATGGCTTTACGAGTCTATACAGAAAGCCTT 601  
QY 325 SerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSer 344  
DB 602 TCAGAGGAAGAAATAGCGGCCCTAAGGCAATATTATTCAAATGATTGACACAGATAACAGT 661  
QY 345 GlyThrLleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeuMet 364  
DB 662 GGAACAATCACATATGAGGAACATAAACAATGTTGTAAGAGATAGGATCTGACTTTAACA 721  
QY 365 GluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAsp 384  
DB 722 GAGTCGGAATCAAGCCTTGATGAGCGCGCTTGACTTTTGACAACAC-GGCATATCGAC 780  
QY 385 Tyr-GlyGluPheLeuAlaAlaThrLeuHisMet 395  
DB 781 TATGGTGAAATTCATCGCTGCAACATTTGCATTG 814

## RESULT 7

CC331661/c

LOCUS

DEFINITION

CC331661

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Ze mays

Ze mays

REFERENCE

AUTHORS

.TITLE

JOURNAL

COMMENT

CONTACT: Cathy Whitelaw

TI GR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@cigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..882

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMMBMA0361M21"

/clone\_lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb

methylation filtered genomic DNA library"

BASE COUNT 129 a 316 c 271 g 166 t

ORIGIN

Alignment Scores:

Pred. No.: 8 55e-114 Length: 882

Score: 1088.50 Matches: 206

Percent Similarity: 82.94% Conservative: 37

Best Local Similarity: 70.31% Mismatches: 49

Query Match: 41.98% Indels: 1

DB: 29 Gaps: 1

US-09-848-806-1 (1-495) x CC331661 (1-882)

QY 132 LysThrLleLeuGlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeu 151

```

Db      980  CGGCTCATCGTCGGCGTCTGGAGCGGTGCCACTCGCTGGCGCTCATGCACCGGACCTC 821
Qy      152  LysProGluAsnPhelLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThrAsp 171
Db      820  AAGCCCGAGAACTCTTGCTCAAGGACAGGGGCCACAGCGGTCTCAAGGCCATCGAC 761
Qy      172  PheGlyLeuSerValPheTyrlsProGlyGlnTyrlsLeuTyrlsAspValValGlySerPro 191
Db      760  TTCGGCTCTCCGCTCTTCTTCAAGCCCGGCGCAGGTGTTCACCGACGCTGGTGGGCTCCCC 701
Qy      192  TyrTyrlsAlaProGluValLeuLysLysCysTyrlsGlyProGluLysLeuAspValTrpSer 211
Db      700  TACTACGTGGCGCGGAGGTGCTGTGCAGCAGCACTACCGGGCCGAGCGGACGTGTGGACG 641
Qy      212  AlaGlyValLeuTyrlsLeuLeuLeuSerGlyValProProPheTyrlsAlaGluThrGlu 231
Db      640  GCGGGGTCTATCGTGTATCATCTCTCTCAGCGGGGTGCGCGGTCTTGGCGGAGCGAC 581
Qy      232  SerGlyLeuPheArgGlnLeuLeuGlnGlyLysLeuAspPheLysSerAspProTrpPro 251
Db      580  CAGGGCATCTTCGACCGCGTGTCTGAAGGGGGCCATCGACTTCGACTCGGAGCGGTGGCG 521
Qy      252  ThrIleSerGluAlaAlaLysAspLeuLeuTyrlsMetLeuGluArgSerProLysLys 271
Db      520  GCCATCTCCAGACGCGCAAGGACCTGATCCGCGAATGCTGGCGTCCGCGCGCGGAC 461
Qy      272  ArgIleSerAlaHisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaAlaPro 291
Db      460  AGGCTGAGCGCGCACCGGTGCTGTGCCACCCGTGGATCTCGCAGAACGGGTGGCCCG 401
Qy      292  AspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLys 311
Db      400  GACAGCGCGTGGACCGCGGTGTCTGACCGGTGAAGCAGTCTCTGGCGCATGAACAG 341
Qy      312  IleLysLysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyGly 331
Db      340  CTCAAGAAGATGCGCTCGCGGTCACTCGCAGAGCTGTCTGGAGAGGAGCTGGCGGG 281
Qy      332  LeuLysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGlu 351
Db      280  CTGAAGGAGATGTCAAGGCGCATGGACACGCGCGGCGGCGCGCCATCACCTTCGACG 221
Qy      352  LeuLysAlaGlyLeuLysArgValGlySer--GluLeuMetGluSerGluLysSer 370
Db      220  CTGAAGGAGGCTGAAGAGGCGCGGTCTCAAGGCTCAGGAGCTCAGGAGGCGGAGATCAGG 161
Qy      371  LeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAspTyrlsGlyGluPheLeuAla 390
Db      160  CTGATGCGCGCGCGCGCATGGACAGAGCGGCGAGCATCGACTACGAGGTTTCGCGC 101
Qy      391  AlaThrLeuHisMetAsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAsp 410
Db      100  GCCACCGTCACATGACGAAGAGGAGCGGCGGAGGACCTGTCTCGCGCATTCGCGCTAC 41
Qy      411  PheAspLysAspGlySerGlyTyrlsThrIleAspGlu 423
Db      40  TTAACACAGACGCGCGGATACATCACCGTCGACGAG 2

```

## RESULT 8

BG596613

LOCUS

DEFINITION EST495291 cSTS Solanum tuberosum cDNA clone cSTS15M13 5' sequence,  
mRNA sequence.

ACCESSION

BG596613

VERSION

BG596613.1

KEYWORDS

SOURCE

ORGANISM

Solanum tuberosum (potato)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
asterids; lamids; Solanales; Solanaceae; Solanum.

REFERENCE

1 (bases 1 to 742) van der Hoeven,R., Bezzerides,J., Sun,H., Cho,J., Chiemingo,A.,

AUTHORS

TITLE  
JOURNAL  
COMMENT

Bougrl,O., Buell,C.R., Ronning,C., Tanksley,S. and Baker,B.  
Generations of ESTs from sprouting potato eyes  
Unpublished  
Contact: Robin Buell  
The Institute for Genomic Research  
9712 Medical Center Dr, Rockville, MD 20850, USA  
Email: potato-array@tigr.org  
This clone can be obtained from the University of Arizona Genomics  
Institute. Orders can be made through URL:  
http://genome.arizona.edu/orders/  
Seq primer: M13F-R.

FEATURES  
source

Location/Qualifiers  
1..742  
/organism="Solanum tuberosum"  
/mol\_type="mRNA"  
/cultivar="Kennebec"  
/db\_xref="taxon:4113"  
/clone="cSTS15M13"  
/tissue\_type="sprouting eyes from tubers"  
/dev\_stage="12-14 weeks post harvest"  
/lab\_host="SOLR"  
/clone\_lib="cSTS"  
/notes="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:  
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were  
taken from tubers. The tubers were incubated at 26C in the  
dark for 2-3 weeks prior to sprouting. The eyes were  
frozen in liquid nitrogen immediately upon removal from  
tubers."  
BASE COUNT 214 a 128 c 181 g 219 t  
ORIGIN  
Alignment Scores:  
Pred. No.: 1 39e-110 Length: 742  
Score: 1059.50 Matches: 196  
Percent Similarity: 89.39% Conservative: 23  
Best Local Similarity: 80.00% Mismatches: 25  
Query Match: 40.86% Indels: 1  
DB: 10 Gaps: 1  
US-09-848-806-1 (1-495) x BG596613 (1-742)

Qy 7 ProArgArgProSerAsnThrValLeuProTyrlsGlnThrProArgLeuArgAspHisTyr 26  
Db 4 CCATTGAAGCCACACA---TTGGTTCTCCCTTACAGAACTGAAAGACTTCAGCAGCTTAC 60  
Qy 27 LeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrTyrlsLeuCysThrGluLys 46  
Db 61 AGTATAGGAAAAAATAATAGGGCAGGCGCAATTTGGAAACCACCCATTTATGTACAGAAAA 120  
Qy 47 SerThrSerAlaAsnTyrlsAlaCysLysSerIleProLysArgLysLeuValCysArgGlu 66  
Db 121 TCACCTGCTACTCTTTATGCTTTCAGAGACTATACCAAGAGAAAGTTGATTGTAAGGAG 180  
Qy 67 AspTyrlsGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGluHisProAsn 86  
Db 181 GATTATGAGGATGTTTGGAGGAGATTTCAGATAATGCACCATTTATCTGAGCACCCCAAT 240  
Qy 87 ValValArgLysGlyThrTyrlsGluAspSerValPheValHisIleValMetGluVal 106  
Db 241 GTGGTCAGATAAAGGGTACTTTATGAAGATACCCCTATATGTGCACATAGTTATGGAGCTT 300  
Qy 107 CysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArgGlu 126  
Db 301 TGTGCTGGTGAGAGACTTTTGTATAGGATCGTTGAAGAGGACATTACAGTGAAGGGA 360  
Qy 127 AlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGlyVal 146  
Db 361 GCTGCGAAGCTTATTAAAACTATTGTGGAGTGGTGAAGGTTGTTCATTCGCTAGGGGTC 420  
Qy 147 MethHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAlaLys 166  
Db 421 ATGCATAGAGACCTCAAACTGAGAAATTTCTTGTCTCAGTTTCAGATTCAGATGCTGCT 480

```

QY 167 LeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyrAsp 186
|||
Db 481 CTTAAGCCACGATTTGGTCTCTCCGTTTCTACACGCCAGGTGAATGTTTCCGAT 540
|||
QY 187 ValValGlySerProTyrTyrValAlaProGluValLeuLysCysTyrGlyProGlu 206
|||
Db 541 GTGGTTGGAAGTCCTTACTATGTGTGACCTGAGTTTACGCAAGCATATGACCTGAA 600
|||
QY 207 IleAspValTrpSerAlaGlyValIleLeuTyrIleLeuSerGlyValProPhe 226
|||
Db 601 TCTGATGTATGGAGCGCAGGAGTATTTGTACATATTACTTAGTGGCGTTCACCTTT 660
|||
QY 227 TrpAlaGluThrGluSerGlyIlePheArgGlnIleGluGlnLysLeuAspPheLys 246
|||
Db 661 TGGCGAAGAACCTGAGATGGGAATATTCGCCAGATATTGCAACAAATAAGATTGAA 720
|||
QY 247 SerAspProTrpPro 251
|||
Db 721 ATCTGACCATGGCCT 735
|||

RESULT 9
BU302783
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU302783 697 bp mRNA linear EST 09-APR-2002
aestivum cDNA clone whyd16m09 5', mRNA sequence.

BU302783.1 GI:20113529
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 697)
Ogiwara, Y. and Murai, K.
Expressed genes in Triticum aestivum
Unpublished
Contact: Tadao Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..697
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="whyd16m09"
/tissue_type="spikelet at late flowering"
/dev_stage="Feekes' scale 6"
/clone_lib="Y. Ogiwara unpublished cDNA library, wh_yd"

BASE COUNT 139 a 200 c 194 g 164 t
ORIGIN

Alignment Scores:
Pred. No.: 4.56e-105 Length: 697
Score: 1011.00 Matches: 182
Percent Similarity: 90.75% Conservative: 24
Best Local Similarity: 80.18% Mismatches: 21
Query Match: 38.99% Indels: 0
DB: 12 Gaps: 0

US-09-848-806-1 (1-495) x BU302783 (1-697)

QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMethHis 80
|||
Db 15 AAGCTGCTGTCCCGCAGACCTACGAGACGCTCGCGCAGATCCAGATCATGCACCAC 74
|||
QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
|||

```

```

Db 75 CTCTCCGACGACCCCAACGTCGTCCGATCCGTGGCGCCTACGAGGACGCGCTCTTCGTG 134
|||
QY 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
|||
Db 135 CACATTGTCTATGAGCTCTGCCCGCGGGAGCTCTTCGACCGCATCTGCGCCAGGGG 194
|||
QY 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
|||
Db 195 CACTACACCGAGCGTCCGCGCAGCTCATCAGGACGATCGTTGGGGTCGTAGAGGCA 254
|||
QY 141 CysHisSerLeuGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160
|||
Db 255 TGGCACTCCTCGCGCTCATGCCCGGACCTCAAGCGGAGAACTTCTCTGTTGCCAGC 314
|||
QY 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
|||
Db 315 ACTGCCGAGGACGCCCACTCAAGACTACCGATTTTCGGGTATCCATGTTCTACAGCCC 374
|||
QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
|||
Db 375 GGTGCAAAATTCCTCTGATGTTGTTGGAGCCCCCTACTATGTTGCACCTGAGGTGCTTCAG 434
|||
QY 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeu 220
|||
Db 435 AAATGCTATGTTCCAGAGCTGATGCTGGAGTCTGGGGTGTATCTGTACATTTTGCTA 494
|||
QY 221 SerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
|||
Db 495 TGTGGCGTCCCCCTTCTGGCGCAGAACTGAAGCAGGAATCTTCAGACAGATCTTCGA 554
|||
QY 241 GlyLysLeuAspPheLysSerAspProTrpProTrpIleSerGluAlaLysAspLeu 260
|||
Db 555 GGCACAACTTGATTTTGGTCTGAGCCCTGAGCTCTCTGACACGCGTAAAGATCTA 614
|||
QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
|||
Db 615 GTCCGTACTATGCTTTGCAGGATCTCTACAAAGCGACTCTCTGCTCATGAGGTCTCTGT 674
|||
QY 281 HisProTrpIleValAspGlu 287
|||
Db 675 CACCCATGATTTGTGATGAT 695
|||

RESULT 10
BU990683
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BU990683.1 GI:22410218
EST.
Lactuca sativa
Lactuca sativa
Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 777)
Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L.,
Lin, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegler, J., Ellison
, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Lai, Z.,
Church, S., Jackson, L. and Bradford, K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
http://compgenomics.ucdavis.edu/
Unpublished
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belong to contig QG_CA_Contig3691, see http://cgdb.ucdavis.edu/
for details.

```



Db	541	AGATTAACTGCACATGAAGTGTTCCTGCGATCTTCAGTTCATGGTGTGGCTCCA	600
Qy	292	AspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLys	311
Db	601	GACAAAGCCTCTGCACCTCTGCGTCTTAAGTCGCATGAACAATTTTACAGCCATGAACAAG	660
Qy	312	lLeLysLysMetAlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyGly	331
Db	661	CTCAAGAAATGCTCTTAGGGTTATAGCGGAGCTTATCGGACGAAGAATA-GCTGGG	719
Qy	332	LeuLysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGlu	350
Db	720	ACTGAACAATGTTTGAGATGATTGATCTGATTAACAGTGGGTCAATTACTTTTGT	776
RESULT 11			
LOCUS	BM779035		
DEFINITION	EST589610 KV2 Medicago truncatula cDNA clone pkV2-22111, mRNA	linear	EST 04-MAR-2002
ACCESSION	BM779035		
VERSION	BM779035.1	GI:19108729	
KEYWORDS	EST.		
SOURCE	Medicago truncatula (barrel medic)		
ORGANISM	Medicago truncatula		
REFERENCE	1 (bases 1 to 813)		
AUTHORS	VandenBosch,K., Endre,G., Hur,J., Beremand,P., Town,C.D., Van Aken		
TITLE	,S., Utterbach,T., Cheung,F., Tsai,J. and Fraser,C.M.		
JOURNAL	ESTs from roots of Medicago truncatula 48 hr after inoculation with		
COMMENT	Sinorhizobium meliloti		
	Contact: VandenBosch K		
	Department of Plant Biology		
	University of Minnesota		
	220 BioSci Center, 1445 Gortner Ave, St. Paul, MN 55108, USA		
	Tel: 612 624 2755		
	Fax: 612 625 1738		
	Email: kvandenb@cbs.umn.edu		
	TIGR sequence name: MTABK54TK More information is available at:		
	www.medicago.org		
FEATURES	Seq primer: SKmod (CTA gaa cta gtc gat cc).		
source	Location/Qualifiers		
	1..813		
	/organism="Medicago truncatula"		
	/mol_type="mRNA"		
	/cultivar="genotype A17"		
	/db_xref="taxon:3880"		
	/clone="pKV2-22111"		
	/tissue_type="Seedling roots"		
	/dev_stage="2 days post-inoculation with Sinorhizobium		
	meliloti"		
	/lab_host="E. coli strain SOLR"		
	/clone_lib="KV2"		
	/note="Vector: pBluescript SK -; Site 1: EcoRI; Site 2:		
	XhoI. cDNA was prepared from polyA+ enriched RNA. The		
	cDNA was directionally ligated into the Unizap XR vector		
	from Stratagene and packaged using Gigapack III Gold		
	packaging extracts. Plasmids containing cDNA inserts		
	were excised from the recombinant lambda-Zap phage using		
	Ex-aassist helper phage and propagated in SOLR cells."		
BASE COUNT	229 a 151 c 188 g 245 t		
ORIGIN			
Alignment Scores:			
Pred. No.:	6.26e-102	Length:	813
Score:	984.50	Matches:	191
Percent Similarity:	83.40%	Conservative:	20
Best Local Similarity:	75.49%	Mismatches:	40
Query Match:	12.97%	Indels:	3
DB:	17	Gaps:	1







```

DEFINITION OSJNEe14E02.f OSJNEE Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEe14E02 5', mRNA sequence.
ACCESSION CB677374
VERSION CB677374.1 GI:29681099
SOURCE EST.
ORGANISM Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 827)
AUTHORS Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
TITLE Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
JOURNAL Unpublished
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtcg
BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: E column: 02
Seq primer: gta aaa cga cgg cca gtcg.
Location/Qualifiers
1..827
/organism="oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEe14E02"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEe"
BASE COUNT 174 a 238 c 231 g 184 t
ORIGIN
XhoI: 24 hrs after inoculation with Rice Blast (70-15)"
174 a 238 c 231 g 184 t

Alignment Scores:
Pred. No.: 6,99e-99 Length: 827
Score: 958.00 Matches: 172
Percent Similarity: 79.27% Conservative: 46
Best Local Similarity: 62.55% Mismatches: 57.
Query Match: 36.95% Indels: 0
DB: 14 Gaps: 0

US-09-848-806-1 (1-495) x CB677374 (1-827)

QY 26 TyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrThrLeuCysThrGlu 45
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
3 TACACCTTCGGCGCGAGCTCGCGCGCGCCAGTTCGGGGTCACCTACCTCGTCCACCC 62
QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
63 AAGGCCACGGGAAGCGCTTCGCTCGAATCCATCGCCACGCGGAGAGCTGCCCCACCGC 122
QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGluHisPro 85
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
123 GACGACATCGAGGAGCTGCGCGGAGGTGCAGATCATGCACCACTCACGGGCCACCGC 182
QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisLeuValMetGlu 105
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
183 AACATCGTCGAGCTCCGGGGCGCTTACGAGGACCCCACTCGGTCAACTCATCATGAG 242
QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

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Db 243 CTCTCGAGGGCGGGAGGCTCTTCGACCCGATCATCGCCAGGGGGGCACTACTCCGAGCGC 302
QY 126 GluAlaValLysLeuLeuLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
303 GCGCGCGCGCGCTCGCGCGGAGATCGTCGCGTGTGTCACAGCTGCCACTCCATGGGG 362
QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
363 GTCTTCACCGGATCTCAAGCGGAACTTTTCTCTCAGTAAAGCGAGGACTCG 422
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
423 CGCTCAAGCCACACTTCGCTCTTCGTTTCTCAAGCTCGGGAGCATTTTAAG 482
QY 186 AspValValGlySerProTyrTyrValAlaProGluValLysLysCysTyrGlyPro 205
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
483 GACCTTGTGGAAGTCGATATATTGTGCACCTGAGTGTGAAACAACTATGGAGCA 542
QY 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuSerGlyValPro 225
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
543 GAGGCTGACATATGAGTGTCTGGCGTATTTTACATCTCTTCTGTGTTCACCT 602
QY 226 PheTTPAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe 245
Db |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
603 TTTTGGCGAGAGTGAAGATGATATTGTGCGGTATTACGTGCTTACGTGCTTAC 662
QY 246 LysSerAspProTyrProThrIleSerGluAlaLysAspLeuIleTyrLysMetLeu 265
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RESULT 15
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LOCUS BQ986998
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QGF11A05.Y9.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
ACCESSION BQ986998
VERSION BQ986998
KEYWORDS EST.
SOURCE Lactuca sativa
ORGANISM Lactuca sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; campanulids; Asterales; Asteraceae; Cichorioideae;
Cichorieae; Lactuca.
1 (bases 1 to 723)
REFERENCE 1
AUTHORS Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegler,J., Ellison
P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
TITLE Lettuce and Sunflower ESTs from the Compositae Genome Project
JOURNAL Unpublished
COMMENT http://compenomics.ucdavis.edu/
Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmunsdon Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-9659
Email: akozik@ucdavis.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QG_CA_Contig3691, see http://cgdb.ucdavis.edu/
for details.
Plate: QGF11 row: A column: 05.
FEATURES
Location/Qualifiers
1..723
/organism="Lactuca sativa"

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GenCore version 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 10:44:32 ; Search time 96 Seconds

(without alignments)  
2275.882 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKENPRPSNTVLPQTP.....KMLNFIADAFVGDGKSD 495

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Delop 6.0 , Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

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Database :

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6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1277.5	49.3	1349	2	US-08-459-448A-20
3	1277.5	49.3	1349	3	US-08-459-595A-20
4	1277.5	49.3	1349	4	US-08-459-504B-20
5	1277.5	49.3	1349	5	US-08-459-444-20
6	1277.5	49.3	1349	6	US-09-547-422-20
7	1159.5	44.7	4162	2	US-08-459-448A-26
8	1159.5	44.7	4162	3	US-08-459-595A-26
9	1159.5	44.7	4162	3	US-08-459-504B-26
10	1159.5	44.7	4162	3	US-08-459-444-26
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12	1159.5	44.7	4165	1	US-07-951-715A-26

13	831	32.0	2374	3	US-09-347-801-3	Sequence 3, Appli
14	771.5	29.8	1400	1	US-08-464-164-1	Sequence 1, Appli
15	771.5	29.8	1400	1	US-08-338-057-1	Sequence 1, Appli
16	771.5	29.8	1400	2	US-08-668-416-1	Sequence 1, Appli
17	623	24.0	2514	3	US-08-655-352-1	Sequence 1, Appli
18	623	24.0	2514	4	US-09-258-016-1	Sequence 1, Appli
19	623	24.0	2514	4	US-09-257-825B-1	Sequence 1, Appli
20	587.5	22.7	1480	4	US-09-016-434-1454	Sequence 1454, Ap
21	582	22.4	1776	3	US-08-655-352-10	Sequence 10, Appl
22	582	22.4	1776	4	US-09-258-016-10	Sequence 10, Appl
23	582	22.4	1776	4	US-09-257-825B-10	Sequence 10, Appl
24	561.5	21.7	1733	4	US-09-620-312D-526	Sequence 526, App
25	558.5	21.5	1694	4	US-09-579-664B-3	Sequence 3, Appli
26	543	20.9	2061	4	US-09-800-960-1	Sequence 1, Appli
27	536	20.7	1282	3	US-08-878-989-12	Sequence 12, Appl
28	536	20.7	1282	3	US-09-272-796-12	Sequence 12, Appl
29	536	20.7	1282	4	US-09-016-434-953	Sequence 953, App
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37	489.5	18.9	2132	3	US-09-186-277-3	Sequence 3, Appli
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45	459.5	17.7	2934	2	US-08-870-693-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1

US-07-951-715A-20  
; Sequence 20, Application US/07951715A  
; Patent No. 5625136

GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlino, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: CIBA-GEIGY Corporation  
STREET: 7 Skyline Drive  
CITY: Hawthorne  
STATE: New York  
COUNTRY: USA  
ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30B

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/951,715A
; FILING DATE: 25-SEP-1992
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1349 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1226
; OTHER INFORMATION: /note= "cDNA sequence for maize
; OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as
; OTHER INFORMATION: disclosed in Figure 30."
; US-07-951-715A-20

Alignment Scores:
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Score: 1277.50 Matches: 242
Percent Similarity: 76.98% Conservative: 59
Best Local Similarity: 61.89% Mismatches: 89
Query Match: 49.27% Indels: 1
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US-09-848-806-1 (1-495) x US-07-951-715A-20 (1-1349)

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RESULT 2
US-08-459-448A-20
; Sequence 20, Application US/08459448A
; Patent No. 5859336
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; APPLICANT: Desai, Nalini M.
; APPLICANT: Lewis, Kelly S.
; APPLICANT: Kramer, Vance C.
; APPLICANT: Warren, Gregory W.
; APPLICANT: Evola, Stephen V.
; APPLICANT: Crossland, Lyle D.
; APPLICANT: Wright, Martha S.
; APPLICANT: Merlin, Ellis J.
; APPLICANT: Launis, Karen L.
; APPLICANT: Rothstein, Steven J.
; APPLICANT: Bowman, Cindy G.
; APPLICANT: Dawson, John L.
; APPLICANT: Dunder, Erik M.
; APPLICANT: Pace, Gary M.
; APPLICANT: Suttle, Janet L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSER: No. 5859336artis Corporation
```

STREET: Patent & Trademark Dept., 520 White Plains

STREET: Rd., POB 2005

CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,448A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA: US 07/772,027

APPLICATION NUMBER: 04-OCT-1991

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

OTHER INFORMATION: pollen-specific calcium dependent protein kinase gene as

OTHER INFORMATION: disclosed in Figure 30."

US-08-459-448A-20

Alignment Scores:

Pred. No.: 3.16e-132 Length: 1349  
Score: 1277.50 Matches: 242  
Percent Similarity: 76.98% Conservative: 59  
Best Local Similarity: 61.89% Mismatches: 89  
Query Match: 49.27% Indels: 1  
DB: 2 Gaps: 1

US-09-848-806-1 (1-495) x US-08-459-448A-20 (1-1349)

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QY 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115  
Db 63 GACAAGCAGAGCGGTGCACCTCGTCATGGAGCTGTGCGCGCGCGGAGCTCTTCGACCG 122  
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QY 156 PheLeuPheAspSerProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175  
Db 243 TTCCTGCTCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTTCGCGCTCTCC 302

QY 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195  
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QY 196 ProGluValLeuLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIle 215  
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QY 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315  
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QY 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyLeuLysGluLeu 335  
Db 723 GCATTGAGGATCATAGCTGGGTGCTTATCCGAAGAGGAGATCACAGGCTGAAGGAGATG 782  
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Db 903 GACGCTGACGCGCAACGGGTAAATTGACTACGAGAAATTCGTACCAGCAACAGTGCATATG 962  
QY 396 AsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGly 415  
Db 963 ACAAACTCGATAGAGAGAGCACCCTTTACACAGCAATTCAGTATTTCGACAGGACAAAC 1022  
QY 416 SerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435  
Db 1023 AGCGGTACATTACTAAAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGTTGTATGAC 1082  
QY 436 Thr---ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454  
Db 1083 GCCGATAAAATCAAGACATCATCTCCGATCGCGACTCTGCACAAATGATGAGGATAGAT 1142  
QY 455 PheSerGluPheThrAlaMetMetArgLysGly 465  
Db 1143 TATTACAGATTGTGGCGATGATGAGAAAGGG 1175

RESULT 3

US-08-459-595A-20

; Sequence 20, Application US/08459595A

; Patent No. 6018104

; GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramer, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.





Db 1143 TATTGAGAGTTTGTGGCGGATGATGAGGAAAGGG 1175

RESULT 4

US-08-459-504B-20

Sequence 20, Application US/08459504B

Patent No. 6075185

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lyle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: NC

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459.504B

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/459.595

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951.715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772.027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

US-08-459-504B-20

Alignment Scores:

Pred. No.: 3.16e-132 Length: 1349

Score: 1277.50 Matches: 242

Percent Similarity: 76.98% Conservative: 59

Best Local Similarity: 61.89% Mismatches: 89

Query Match: 49.27% Indels: 1

DB: 3 Gaps: 1

US-09-848-806-1 (1-495) x US-08-459-504B-20 (1-1349)

QY 76 GlnIleMetHisHisLeuSerGluHisProAenValValArgIleLysGlyThrTyrGlu 95

DB 3 CAGATCATGCACCACTCTCCGGCCAGCCCAACGTGGTGGGCTCCGGCGCGTACGAG 62

QY 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115

DB 63 GACAAGCAGAGCGTGCACCTCTGTCATGAGCTGTCCGGGGGGGAGGCTCTTCACCCG 122

QY 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuLysThrIleLeu 135

DB 123 ATCATCGCCCGGGCCAGTACACGAGCGCGCGCGCGGAGCTCTGCGGCCCATCGTG 182

QY 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAen 155

DB 183 CAGATCGTGCACACCTGCCACTCTCCATGGGGGTGATGCACCGGACATCAAGCCCGAGAAC 242

QY 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175

DB 243 TTCTCTGTCTCAGCAGGAGGAGCGCGCGCTCAAGGCCACCGACTCTCGGCTCTCC 302

QY 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195

DB 303 GTCTTCTTCAAGGAGGGGCGAGCTGCTCAGGGACATCTGTCGCGAGCGCTACTACATCGCG 362

QY 196 ProGluValLeuLysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIle 215

DB 363 CCCGAGGTGCTCAAGAGGAAGTACGGCCCGGAGCGGCACATCTGGAGCGTTCGGCGTCATG 422

QY 216 LeuTyrIleLeuLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePhe 235

DB 423 CTCTACATCTTCTCGCGGGGTGCTCCCTTCTGGGCAGAGAACGAGAACGGGATCTTC 482

QY 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTyrProThrIleSerGlu 255

DB 483 ACCGCCATCTTCGAGGGGCGAGCTTGACCTCTCCAGCGAGCCATGCGCCACATCTCGCG 542

QY 256 AlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAla 275

DB 543 GGAGCCCAAGGATCTGCTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCACGGCG 602

QY 276 HisGluAlaLeuCysHisProTyrIleValAspGluGlnAlaAlaProAspLysProLeu 295

DB 603 TTCAGGTCTCAATCACCCATGATCAAGAGACGGAGCGCGCTGACACGCCGCTT 662

QY 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315

DB 663 GACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCCATGAACCATTTCAAGAAAGCA 722

QY 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeu 335

DB 723 GCATTGAGGATCATAGCTGGGTGCTTATCCGAAGGAGATCACAGGGCTGAAGGAGATG 782

QY 336 PheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGly 355

DB 783 TTCAGAACATTGACAGGATTAACAGCGGGGACCAATTACCTTCGACGAGCTCAACACCGGG 842

QY 356 LeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAla 375

DB 843 TTGCAAAAGCAGCGGCCCAAGCTGTACAGACAGCGAAATGGAGAACTAATGGAAGCAGCT 902

QY 376 AspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHiMet 395

DB 903 GACGCTGACGGCAACGGGGTTAATTGCTACGAGCAATTCGTCCACCGCAACAGTCATATG 962



Db 843 TTGGCAAGACGGCCCAAGCTGTGACAGACGCGAAATGGAGAACTAATGGAAGCAGCT 902  
Qy 376 AspileAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaIleThrLeuHisMet 395  
Db 903 GACGCTGACCGCAACGGGTTAATTGACTACGCAATTCGTACCGCAACAGTGCAATG 962  
Qy 396 AsnLysMetGluArgGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGly 415  
Db 963 AACAACTGGATAGAGAAGACCTTTACACAGCATTCAGTATTTCGACAAAGGACAAC 1022  
Qy 416 SerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435  
Db 1023 AGCGGGTACATTACTAAAGAGAGCTTGACGACCGCTTGAAGGAGCAAGGGTTGTATGAC 1082  
Qy 436 Thr----ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454  
Db 1083 GCCGATAAATCAAGACATCATCTCGATGCCGACTCTGACATGATGAGGATAGAT 1142  
Qy 455 PheSerGluPheThrAlaMetMetArgLysGly 465  
Db 1143 TATTTCAGAGTTTGTGGCGATGATGAGGAAAGGG 1175

## RESULT 6

US-09-547-422-20  
; Sequence 0, Application US/09547422  
; Patent No. 6320100  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.  
; Warren, Gregory W.  
; Evola, Stephen V.  
; Crossland, Lytle D.  
; Wright, Martha S.  
; Merlin, Ellis J.  
; Launis, Karen L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/547,422  
; FILING DATE: 11-Apr-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/459,595  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-18805H  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: /note= "cDNA sequence for maize  
; pollen-specific calcium dependent protein kinase gene as

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1349 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..1226  
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:  
US-09-547-422-20  
Alignment Scores:  
Pred. No.: 3,16e-132 Length: 1349  
Score: 1277.50 Matches: 242  
Percent Similarity: 76.98% Conservative: 59  
Best Local Similarity: 61.89% Mismatches: 89  
Query Match: 49.27% Indels: 1  
DB: 4 Gaps: 1

US-09-848-806-1 (1-495) x US-09-547-422-20 (1-1349)

Qy 76 GlnIleMetHisHisLeuSerGluHisProAsnValValArgIleLysGlyThrTyrGlu 95  
Db 3 CAGATCATGCACCACTCTCCGGCCAGCCCAACGTGTGGCCCTCCGCGCGGTACGAG 62  
Qy 96 AspSerValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArg 115  
Db 63 GACAAGCAGAGCGTGCACCTCGTCATGGAGCTGTGCGCGGGCGGGAGCTCTTCGACCGC 122  
Qy 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135  
Db 123 ATCATCGCCGGGGCCAGTACACGGAGCGCGCGCGAGCTGTGCGCGCCATCGTG 182  
Qy 136 GlyValValGluAlaCysHisSerLysLeuGlyValMetHisArgAspLeuLysProGluAsn 155  
Db 183 CAGATCGTCACACCTGCCACTCCATGGGGGTGATGACCGGAGCATCAAGCCGCGAGAAC 242  
Qy 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175  
Db 243 TTCTCTCTCTCAGCAAGGACGAGGACGCGCGCTCAAGGCCACCGACTTCGGCCTCTCC 302  
Qy 176 ValPheTyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAla 195  
Db 303 GTCTTCTTCAGAGGGCGAGCTGCTCAGGGACATCGTCGCGAGCCCTACTACATCGCG 362  
Qy 196 ProGluValLeuLysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIle 215  
Db 363 CCGAGGTGCTCAAGAGGAAGTACGGCCCGGAGGCGGACATCTGGAGCGTCGGCGTCATG 422  
Qy 216 LeuTyrIleLeuLeuSerGlyValProPheThrAlaGluThrGluSerGlyIlePhe 235  
Db 423 CTCTACATCTCTCGCGCGTGTCTCTCTGCGGACAGAAACGAGAACGAGCATCTTTC 482  
Qy 236 ArgGlnIleLeuGlnGlyLysLeuAspPheLysSerAspProTyrProThrIleSerGlu 255  
Db 483 ACGGCATCTCGAGGGCGAGCTTACCTCTCCAGCGAGCCATGGCCACACATCTCGCGG 542  
Qy 256 AlaAlaLysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAla 275  
Db 543 GGAGCCAAAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGG 602  
Qy 276 HisGluAlaLeuCysHisProTrpIleValAspGluGlnAlaAlaProAspLysProLeu 295  
Db 603 TTCCAGGTCTCAATCACCCATGGATCAAGAAGACGGAGACGCGCTCACACCGCGCTT 662  
Qy 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315  
Db 663 GACAACGTTGTTCTCGACAGGCTCAAGCAGTTTCAGGGCGCATGAACAGTTCGAAGAAGCA 722  
Qy 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeu 335

; disclosed in Figure 30."

Db 723 GCATTGAGTATCATAGCTGGGTGCTATCCGAAGAGGAGATCAGGGCTGAAGAGATG 782  
Qy 336 PheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGly 355  
Db 783 TTCAGAAACATGTACAAGTAACACAGCGGACCATATTACCTCGAGAGCTCAAAACACGGG 842  
Qy 356 LeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaLa 375  
Db 843 TTGCAAGACGCGGCCCAAGCTGTACAGACGCAATGGAGAACTAATGGAAGCAGCT 902  
Qy 376 AspIleAspAsnSerGlyThrIleAspTyrGlyGluPheLeuAlaLaThrLeuHisMet 395  
Db 903 GACGCTGACGCAACGGGTAAATTGACTACGACGAATTCGTCACCGCAACAGTGCATATG 962  
Qy 396 AsnLysMetGluArgGluGluIleuValalalalalalalalalalalalalalalal 415  
Db 963 AACAACTGGATAGAGAGACACCTTTACACAGCATTTCCAGTATTTTCGACAGGACAAC 1022  
Qy 416 SerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435  
Db 1023 AGCGGTACATTACTAAGAGAGAGCTTGAGCAGCCTTGAAGAGCAAGGTTGTATGAC 1082  
Qy 436 Thr---ProLeuAspAspMetIleLysGluIleAspLeuAspAsnAspGlyLysIleAsp 454  
Db 1083 GCCGATAAAATCAAAGACATCATCTCCGATCCCGACTCTGACATGATGGAAGATAGAT 1142  
Qy 455 PheSerGluPheThrAlaMetMetArgLysGly 465  
Db 1143 TATTACAGATTGTGGCGCATGATGAGGAAGGG 1175

RESULT 7

US-08-459-448A-26  
; Sequence 26, Application US/08459448A  
; Patent No. 5859336  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; APPLICANT: Desai, Nalini M.  
; APPLICANT: Lewis, Kelly S.  
; APPLICANT: Kramer, Vance C.  
; APPLICANT: Warren, Gregory W.  
; APPLICANT: Evola, Stephen V.  
; APPLICANT: Crossland, Lyle D.  
; APPLICANT: Wright, Martha S.  
; APPLICANT: Merlin, Ellis J.  
; APPLICANT: Launis, Karen L.  
; APPLICANT: Rothstein, Steven J.  
; APPLICANT: Bowman, Cindy G.  
; APPLICANT: Dawson, John L.  
; APPLICANT: Dunder, Erik M.  
; APPLICANT: Pace, Gary M.  
; APPLICANT: Suttie, Janet L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 5859336artis Corporation  
; STREET: Patent & Trademark Dept., 520 White Plains  
; STREET: Rd., POB 2005  
; CITY: Tarrytown  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10591-9005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/459,448A  
; FILING DATE: 02-JUN-1995  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pace, Gary M.  
; REGISTRATION NUMBER: 40403  
; REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8582  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4162 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1418..1427  
; OTHER INFORMATION: /note= "start of mRNA"  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 1481..2366  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 2367..2451  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 2452..2602  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 2603..2690  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 2691..2804  
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; NAME/KEY: intron  
; LOCATION: 2805..2906  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 2907..3075  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 3076..3177  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 3178..3304  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 3305..3398  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 3399..3498  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 3499..3713  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 3714..3811  
; FEATURE:  
; NAME/KEY: promoter  
; LOCATION: 1..1477  
; IDENTIFICATION METHOD: experimental  
; OTHER INFORMATION: /partial  
; OTHER INFORMATION: /function= "pollen-specific promoter region"  
; OTHER INFORMATION: /evidence= EXPERIMENTAL  
; US-08-459-448A-26

Alignment Scores:

Pred. No.:	2.31e-118	Length:	4162
Score:	1159.50	Matches:	276
Percent Similarity:	50.00%	Conservative:	69
Best Local Similarity:	40.00%	Mismatches:	115
Query Match:	44.72%	Indels:	235
DB:	2	Gaps:	7
US-09-848-806-1 (1-495) x US-08-459-448A-26 (1-4162)			
QY	6	AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis	25
DB	1698	AACCGCGCGCGCGTG-GGCACGGTGTGGCGCGGCCATCGGAGGACGTGGCGCGACC	1756
QY	26	TyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrTyrLeuCysThrGlu	45
DB	1757	TACTCGATGGGCAAGAGCTCGGCGCGGCGAGTTGGCGGTGACGCACCTGTGCACGCAC	1816
QY	46	LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg	65
DB	1817	CGGACGCGCGGAGAACCTGGCTGCGAAGCATCGGAGCGAAGCTGGCGCCGAGG	1876
QY	66	GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHisLeuSerGluHisPro	85
DB	1877	GAGGACGTGGACGAGCTGCGCGCGGAGGTGCAGATCATGCACCACTCTCCGGCCAGCCC	1936
QY	86	AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu	105
DB	1937	AACGTGTGGGCTCTCGCGCGCGGTACGAGGACAAAGCAGACGTGCACCTCGTCATGGAG	1996
QY	106	ValCysGluGlyGlyLeuLeuPheAspArgIleValSerLysGlyHisPheSerGluArg	125
DB	1997	CTGTGCGCGCGGGGAGCTCTTCGACCGCATCATCGCCCGGGCGCAGTACACGGAGCGC	2056
QY	126	GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly	145
DB	2057	GGCGCGCGGAGCTGCTCGCGCCATCGTGAGATCGTGACACCTGCCACTCCATGGG	2116
QY	146	ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla	165
DB	2117	GTGATGCACCGGACATCAACGCCGAGAACTCTCTGCTGTCTCAACAAGGACGAGACGCG	2176
QY	166	LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr	185
DB	2177	CCGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTTCTCAAGGAGGCGAGCTGCTCAGG	2236
QY	186	AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro	205
DB	2237	GACATCGTCGCGAGCGCTACTACATCGCGCGGAGGTGTCTCAAGAGAAAGTACGCGCGC	2296
QY	206	GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuSerGlyValProPro	225
DB	2297	GAGCCGACATCTGAGCGTCGGGCTCATGCTCTACATCTTCTTCGCGCGGCTGCTCCC	2356
QY	226	PheTrpAla-----	228
DB	2357	TTCTGGGC-AGGTCCGATCCGTCGCTGCTCTAGACGATATACAGAACCCGACGATG	2415
QY	229	-----GluThrGluSerGlyIlePheArgGln	237
DB	2416	GATTTGCTTCTCAGCCCTGTTCTTTGCATCACCAAGAACGAGACGCGATCTTTCACCGCC	2475
QY	238	IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAla	257
DB	2476	ATCTTCGAGGGGAGCTTGACCTCTCCAGCGAGCCATGGCCACACATCTCGCGGGAGCC	2535
QY	258	LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu	277
DB	2536	AAGGATCTCGTCAAGAAGATGCTCAACATCAACCAAGGAGCGGCTCACGCGGTCCAG	2595
QY	278	AlaLeuCys-----	280
DB	2596	GTCCTCAG-TAAGTACCAGATCGTGTCTGCATACACTCATATGAATTGTATGCTTCAT	2654

Db 3733 AGAGTTTGGCGATGATGAGGAAGGG 3760

RESULT 8

US-08-459-595A-26

Sequence 26, Application US/08459595A

Patent No. 6018104

GENERAL INFORMATION:

APPLICANT: Koziel, Michael G.

APPLICANT: Desai, Nalini M.

APPLICANT: Lewis, Kelly S.

APPLICANT: Kramer, Vance C.

APPLICANT: Warren, Gregory W.

APPLICANT: Evola, Stephen V.

APPLICANT: Crossland, Lytle D.

APPLICANT: Wright, Martha S.

APPLICANT: Merlin, Ellis J.

APPLICANT: Launis, Karen L.

APPLICANT: Rothstein, Steven J.

APPLICANT: Bowman, Cindy G.

APPLICANT: Dawson, John L.

APPLICANT: Dunder, Erik M.

APPLICANT: Pace, Gary M.

APPLICANT: Suttie, Janet L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6018104artis Corporation

STREET: Patent & Trademark Dept., 520 White Plains

STREET: Rd., POB 2005

CITY: Tarrytown

STATE: New York

COUNTRY: USA

ZIP: 10591-9005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,595A

FILING DATE: 02-JUN-1995

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403

REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3

TELEPHONE: (919)541-8582

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 26:

SEQUENCE CHARACTERISTICS:

LENGTH: 4162 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: misc feature

LOCATION: 1418..1427

OTHER INFORMATION: /note= "start of mRNA"

FEATURE:

NAME/KEY: exon

LOCATION: 1481..2366

FEATURE:

NAME/KEY: intron

LOCATION: 2367..2451

FEATURE:

NAME/KEY: exon

LOCATION: 2452..2602

FEATURE:

NAME/KEY: intron

LOCATION: 2603..2690

FEATURE:

NAME/KEY: exon

LOCATION: 2691..2804

FEATURE:

NAME/KEY: intron

LOCATION: 2805..2906

FEATURE:

NAME/KEY: exon

LOCATION: 2907..3075

FEATURE:

NAME/KEY: intron

LOCATION: 3076..3177

FEATURE:

NAME/KEY: exon

LOCATION: 3178..3304

FEATURE:

NAME/KEY: intron

LOCATION: 3305..3398

FEATURE:

NAME/KEY: exon

LOCATION: 3399..3498

FEATURE:

NAME/KEY: intron

LOCATION: 3499..3713

FEATURE:

NAME/KEY: exon

LOCATION: 3714..3811

FEATURE:

NAME/KEY: promoter

LOCATION: 1..1477

IDENTIFICATION METHOD: experimental

OTHER INFORMATION: /partial

OTHER INFORMATION: /function= "pollen-specific promoter region"

OTHER INFORMATION: /evidence= EXPERIMENTAL

US-08-459-595A-26

Alignment Scores:

Pred. No.: 2,31e-118 Length: 4162

Score: 1159.50 Matches: 276

Percent Similarity: 50.00% Conservatives: 69

Best Local Similarity: 40.00% Mismatches: 115

Query Match: 44.72% Indels: 235

DB: 3 Gaps: 7

US-09-848-806-1 (1-495) x US-08-459-595A-26 (1-4162)

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Db 1698 AACCGCGCGCGCGCTG-GGCACGGTCTGGCGCGCCCATGGAGGACGTGGCGCGAC 1756

QY 26 TyrlLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrlLeuCysThrGlu 45

Db 1757 TACTCGATGGCAAGGAGCTCGGCGCGCGGCGAGTTCGGCGTGCACGACCTGTGCACGCGAC 1816

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QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125  
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Db 2177 CCGCTCAAGCCACCGACTTCGGCTCTCGCTCTCTTCAAGGAGGCGAGCTCGCTCAGG 2236  
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QY 229 -----GluThrGluSerGlyIlePheArgGln 237  
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QY 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277  
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QY 278 AlaLeuCys 280  
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QY 281 -----HisProTrpIleValAspGluGln 288  
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QY 289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308  
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QY 309 MetAsnLysIleLysLysMetAlaLeuArgVal 319  
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Db 2835 CAACTTCTGAGAACAGCAATGCTTACCGGAGAAATTTTCATTATTAATGCTCTTGATG 2894  
QY 320 -----TleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGlu 334  
Db 2895 ACATAATGTTAGATCATAGTGGTGCCTATCCGAAGAGGAGATCACAGGCTGAGAGGAG 2954  
QY 335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla 354  
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QY 355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla 374  
Db 3015 GGGTGGCAAGACGCGGCGCCAGCTGTGACAGCGCAATGGAGAACTAATGGAGCA 3074

QY 374 ----- 374  
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QY 375 -----AlaAspIleAspAsnSe 380  
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Db 3195 CGGGTTAAATTGACTAGACGAATTCGTCCACCGCAACAGTGCATATGAACAACTGGATAG 3254  
QY 400 gGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly 417  
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## RESULT 9

US-08-459-504B-26

; Sequence 26, Application US/08459504B

; Patent No. 6075185

## GENERAL INFORMATION:

; APPLICANT: Koziel, Michael G.

; APPLICANT: Desai, Nalini M.

; APPLICANT: Lewis, Kelly S.

; APPLICANT: Kramet, Vance C.

; APPLICANT: Warren, Gregory W.

; APPLICANT: Evola, Stephen V.

; APPLICANT: Crossland, Lyle D.

; APPLICANT: Wright, Martha S.

; APPLICANT: Merlin, Ellis J.

; APPLICANT: Launis, Karen L.

; APPLICANT: Rothstein, Steven J.

; APPLICANT: Bowman, Cindy G.

; APPLICANT: Dawson, John L.

; APPLICANT: Dunder, Erik M.

; APPLICANT: Pace, Gary M.

; APPLICANT: Suttie, Janet L.

; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

; NUMBER OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE

; NUMBER OF SEQUENCES: 94

; CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6075185artis Corporation  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709  
COMPUTER: IBM PC compatible  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459,504B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/459,595  
FILING DATE: 02-JUN-1995  
APPLICATION NUMBER: US 07/951,715  
FILING DATE: 25-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/772,027  
FILING DATE: 04-OCT-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Meigs, J. Timothy  
REGISTRATION NUMBER: 38,241  
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919)541-8587  
TELEFAX: (919)541-8689  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4162 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 1418..1427  
OTHER INFORMATION: /note= "start of mRNA"  
FEATURE:  
NAME/KEY: exon  
LOCATION: 1481..2366  
FEATURE:  
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US-08-459-504B-26  
Alignment Scores:  
Pred. No.: 2,31e-118 Length: 4162  
Score: 1159.50 Matches: 276  
Percent Similarity: 50.00% Conservatives: 69  
Best Local Similarity: 40.00% Mismatches: 115  
Query Match: 44.72% Indels: 235  
DB: 3 Gaps: 7  
US-09-848-806-1 (1-495) x US-08-459-504B-26 (1-4162)  
Qy 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25  
Db 1698 AACCGCGCGCGCGGTG-GGCACGGTGTCTGGCGCGCCCATGGAGGACGTGCGCGCGACC 1756  
Qy 26 TyrLeuLeuGlyLysLysLeuGlyGlnPheGlyThrThrTyrLeuCysThrGlu 45  
Db 1757 TACTCGATGGGCAAGAGGTCTGGCGCGGGCAGTTTCGGCGTGCACGACCTGTGCACGCAC 1816  
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Qy	278	AlaLeuCys		280
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Db	2715	GACGCGCTGACACGCGCTTGACAACGTTGTTCTCGACAGGCTCAAGCAGTTCAGGCCC	2774	
Qy	309	MetAenLysIleLysLysMetAlaLeuArgVal		319
Db	2775	ATGAACGATTCAGAAAGCAGCAATGAGGGTACATTCGTATAAAGCTCCACAAATA	2834	
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Qy	320			334
Db	2895	ACATAATGTTAGATCATAGCTGGGTGCTATCCGAGAGGAGATCACAGGCTGAAGGAG	2954	
Qy	335	LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla	354	
Db	2955	ATGTTCAAGAACAATGACAGGATTAACAGCGGAGCAATACCTTCGACGAGCTCAACAC	3014	
Qy	355	GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla	374	
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Qy	374			374
Db	3075	GTGAGTTTTCAGAGTACAATCTTAAAAAAGGAATTGTGATCTTTTCAAAATGAAGAAG	3134	
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Qy	400	gGluGluIleuValAlaIaPheSerAspPheAspLysAspGlySerGly	417	
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Db 3553 ATCATGATATCAAAATTTTGAGGTGGCGGTGCTTACAGAAATAGAACCCAGTACACCAAAAT 3613
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RESULT 10
US-08-459-444-26
; Sequence 26, Application US/08459444A
; Patent No. 6121014
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Lounis, Karen L.
; TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
; NUCLEIC ACID CODING SEQUENCE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, I
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,444A
; FILING DATE: 02-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805/P1/CGC1577/CIP/DIV6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:

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Db 3195 CCGGTTAATTCATGACGCAATTCGTCACCGCAACAGTCATATGAACAACTGGATAG 3254
QY 400 gGluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGly----- 417
Db 3255 AGAAGAGCACCTTTACACAGCATTTCCAGTATTTTCGACACAGGACACACAGCGG-GTAAGTTG 3313
QY 417 ----- 417
Db 3314 AACGTTAAATGATACAGCTGGTACCTGAATTTCTGGACACACATATCATACAGGACAC 3373
QY 418 -----TyrlleThrIleAspGluLeuGlnSerAlaCysTh 429
Db 3374 ATATATAATTCGTTTATCTCACAGGTACATTAATAAGAGAGCTTGAGCACGCTTGAA 3433
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RESULT 11
US-09-547-422-26
; Sequence 26, Application US/09547422
; Patent No. 6320100
; GENERAL INFORMATION:
; APPLICANT: Koziel, Michael G.
; Desai, Nalini M.
; Lewis, Kelly S.
; Kramer, Vance C.
; Warren, Gregory W.
; Evola, Stephen V.
; Crossland, Lyle D.
; Wright, Martha S.
; Merlin, Ellis J.
; Launis, Karen L.
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
; INSECTICIDAL ACTIVITY IN MAIZE
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6320100artis Agribusiness Biotechnology Research, Inc.
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/547,422
; FILING DATE: 11-Apr-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/459,595
; FILING DATE: 02-JUN-1995
; APPLICATION NUMBER: US 07/951,715
; FILING DATE: 25-SEP-1992
; APPLICATION NUMBER: US 07/772,027
; FILING DATE: 04-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: S-18805H
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8587
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1418..1427
; OTHER INFORMATION: /note= "start of mRNA"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1481..2366
; FEATURE:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-547-422-26
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Alignment Scores:

Pred. No.:	2,31e-118	Length:	4162
Score:	1159.50	Matches:	276
Percent Similarity:	50.00%	Conservative:	69
Best Local Similarity:	40.00%	Mismatches:	115
Query Match:	44.72%	Indels:	235
DB:	4	Gaps:	7

US-09-848-806-1 (1-495) x US-09-547-422-26 (1-4162)

Qy	6	AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis	25
Db	1698	AACCGGCGGCGCGTG-GGCACGGTGTGGCGCGGCCCATGGAGGAGTGTCTCGCGAC	1756

Qy	26	TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGlu	45
		.....	
Db	1757	TACTCGATGGGCAAGAGACTTCGGCGCGCGGACTTCGGCGGTACCGACTTGGCAGCCAC	1816

46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65

Db	1817	CGACGACGCGCGAGAAAGCTGGCGTGCAGAGACGATCGCGAAGCGGAAGCTGGCGGCCAGG	1876
Qy	66	GluAspTyrGluAspValTrpArgGluLeuGlnIleMetHisHisLeuSerGluHispro	85

DB	1877	GAGGACGTGGACGACGTGGCGGGAGGTGCAGATCATGCACACCTCTCCGGCCAGCC	1936
QY	86	AanValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu	105

Db	1937	AACGTGTGGGCTCCGGCGCGTACGAGCAAGCAGAGCGGTGCACCTCTCATGGAG	1996
		.....:::	
Qy	106	ValCysGluGluGluGluLeuPheAspArgIleValSerIleGluHisPheSerGluArg	125

[illegible]

Qy 126 GluAlaValLysLeuIleLysThrIleLeuGlyValGluAlaCysHisserLeuGly 145  
Db 2057 GGCGCGCGAGCTGCTGGCGCCATCGTGCAGATCGTGACACCTGCCATCCATGGG 2116

QY	146	ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAla	165
		.....:::.....	
Db	2117	GTCATGCACCGGGACATCAGCCCCGAGAACTTCCTGCTCAGCAAGGAGAGGACGCG	2176

Oy		166	LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr	185
Dδ		2177	CCGCCTCAAGGGCACCCGACTTCGGCCCTCCGCTCTTCTCAAGGAGGCCGAGCTGTCTCAGG	2236

[illegible][illegible]

Db	2297	GAGCGGACATCTGGAGCGTCGGCGTCATGCTCTACATCTTCTCGCCGGCGTGCCTCCC	2356
Qy	226	PheTtpAla 	228

	TTCCTGGGC	-AGTCCGATCCGTCCGTTTCCTCCTAGACGATATACAGAACC	CGACGATG	2415
Db	2357			
	-----	GluThrGluSerGluValIlePheAraGln	237	
QY	229			

[illegible]

D<sub>b</sub>

2476 ATCTGCGAGGGCAGCTTGACTCTCCAGGAGGCCATGGCCACACATCTCGCCGGAGCC 2535

QY	LysAspLeuIleTyrLysMetLeuGluArgSerProLysValysArgIleSerAlahisGlu	277
	.....:::	
Db	AAGGATCTCGTCAGAAGATGCTCAACATCAACCCTAAGACGGGTCCAGCGTTCCAG	2595

Qy 278 AlaLeuCys-----280  
          |||

2596	Db	GTCCTCAG - TAAAGTACCAGGATCGTTGCTGCTCATACACTCATATGAATTTGATTCGTTTCAT	2655
281	Qy	-----HisProTirpIleValAaspGluGln	288
2655	Db	GAGCAACGATCGAGCGGATTTGGTGAACTTGTAGATCACCCATGGATCAAAGAAGACGGGA	2714
289	Qy	AlaAlaProAplysProLeuAaspProAlaValLeuSerArgLeuIlysGlnPheSerGln	308
2715	Db	GACGCGCTGACACGCGCTTGACAACGGTTGTCTCGACAGGCTCAAGCAGTTTCAGGGCC	2774
309	Qy	MetAenLybIleLybIlysMetAlaLeuAaGVal	319
2775	Db	ATGACCGATTCAAGAAAGCAGCATTTGAGGGTACATTACTGTATAAAGCTCCACAAATA	2834
319	Qy	-----	319
2835	Db	CAACTTCTGAAGAACAGCAATGCTTACAGCGCAGAATTTTCATTATATAATGCTCTTGATG	2894
320	Qy	-----IleAlaGluArgLeuSerGluGluIleGlyGlyLeuIlysGlu	334
2895	Db	ACATAATGTTAGATCATAGCTGGTGCTCTATCCGAAGAGGAGATCACAGGGCTGAAGGAG	2954
335	Qy	LeuPheIlysMetIleAaspThrAaspAenSerGlyThrIlePheGluGluIleIlysAla	354
2955	Db	ATGTTCAAGAACATTGACAAGGATAACAGCGGACCATTACCCTCCAGCAGGTCAACAC	3014
355	Qy	GlyLeuIysArgValGlySerGluLeuMetGluSerGluIleIlysSerLeuMetAaspAla	374
3015	Db	GGGTTGGCAAGCACGGGCCCAAGCTGTACAGACGGCAATGGAGAAACTAATGGGAAGCA	3074
374	Qy	-----	374
3075	Db	GTGAGTTTTCAGAGTACAATCTTAAAAAAGAAATGTGATCTCTTTTCAAAATGAAGAAG	3134
375	Qy	-----AlaAaspIleAaspAenSe	380
3135	Db	TAATCTGAANAACATCCCTGCTGAAATGCTTTTATACATTCTCCAGGCTGACGCTCAGCGCAA	3194
380	Qy	rGlyThrIleAaspTyxGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluAr	400
3195	Db	CGGTTAAATTGACTACGACGAATTCGTACCGCAACAGTGCATATGAACAAACTGGATAG	3254
400	Qy	gGluGluIleLeuValAlaAlaPheSerAaspPheAplysAaspGlySerGly	417
3255	Db	AGAAGACACCTTTTACAGACCATTCACAGTATTCGACAGGACACACAGCGG - GTAAGTTG	3313
417	Qy	-----	417
3314	Db	AACGTTAAATGATGATCAGCTGGTACTCGAATTTCTGGCAACACATATCATATACAGGACAC	3373
418	Qy	-----TyrIleThrIleAaspGluLeuGlnSerAlaCysTh	429
3374	Db	ATATATAATTGCTTTATCTCACAGGTACATTACTTAAGAAGAGCTTGACACGCTTGAA	3433
429	Qy	rGluPheGlyLeuCyAaspThr - - - ProLeuAaspAaspMetIleIlysGluIleAaspLeuAs	448
3434	Db	GGAGCAAGGGTTGTATGACGCCGATATAAAATCAAGACATCATCTCCGATGCCGACTCTGA	3493
448	Qy	pAen - - - - -	449
3494	Db	CAA - TGTAAGGAACAACAATTATTTAAATTTTCAGCCGACAAACTAAACTATAGAAACCAC	3552
449	Qy	-----	449
3553	Db	ATCATGATATCAAAATTTTTCAGGTGGGGTGCTTACAGAAATAGAACCCAGTACACCAAAAT	3612
449	Qy	-----	449
3613	Db	GACTAACTTGTCATGATTAGTTGTTCTCGTAACTGAACATTTGTGTTCTTAGTTTCTTA	3672
450	Qy	-----AepGlyIysIleAaspPheSe	456
3673	Db	TTGTTAAACCAAGACTTAAATTCATTCTTTTGACATGACAGGATGGAAGATAGATTATTC	3732

:	FEATURE:				
:	NAME/KEY:	exon			
:	LOCATION:	2450...2602			
:	FEATURE:				
:	NAME/KEY:	intron			
:	LOCATION:	2603...2688			
:	FEATURE:				
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:	NAME/KEY:	intron			
:	LOCATION:	3498...3712			
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:	NAME/KEY:	exon			
:	LOCATION:	3713...3811			
US-07-951-715A-26					
Alignment Scores:					
Pred. No.:	2.32e-118	Length:	4165		
Score:	1159.50	Matches:	276		
Percent Similarity:	50.00%	Conservative:	69		
Best Local Similarity:	40.00%	Mismatches:	115		
Query Match:	44.72%	Indels:	235		
DB:	1	Gaps:	7		
US-09-848-806-1 (1-495) x US-07-951-715A-26 (1-4165)					
Qy	6	AsnProArgArgProSerAnThrValLeuLeuProTyrGlnThrProArgLeuArgAspHis	25		
Db	1696	AACCGGGCGGGCGCGTG-GGCACGGTGCTGGCGGCCCATGGAGGACGTGGCGCGCACC	1754		
Qy	26	TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCyeThrGlu	45		
Db	1755	TATCGATGGCAAGAGACTTGGGGCGGGCAGTTGGCGTGACGCACCTGTGCACGCAC	1814		
Qy	46	LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg	65		
Db	1815	CGGACGAGCGCGGAGAAGCTGGCGTCAAGACGATCGGAAGCGGAAGCTGGCGGCCAGG	1874		
Qy	66	GluAspTyrGluAspValTrpArgGluIleGlnIleMethHisHisLeuSerGluHisPro	85		
Db	1875	GAGGACGTGACGACCGTCGGCGGGGAGGTGCAGATCATGCACCACTCTCCGGCCAGCCC	1934		
Qy	86	AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu	105		
Db	1935	AACGTGGTGGGCTCCGCGCGCGGTACGAGGACAAGACGAGCGGTGCACCTCGTCATGGAG	1994		
Qy	106	ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg	125		
Db	1995	CTGTGGCGGGCGGGGAGCTTTCGACCGCATCATCGCCCGGGGCCAGTACACGAGCGC	2054		
Qy	126	GluAlaValLysLeuIleLysThrIleLeuGlyValValCluaLaCysHisSerLeuGly	145		
Db	2055	GGCGCCGCGAGCTGTCTGGCGGCCATCTGTGCATCTGTGCACACCTGCCATCTCATTTGGG	2114		

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Qy 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165
Db 2115 GTGATGACCGGGACATCAAGCCGAGAACTTCCTGCTGCACGACGAGGACGCG 2174
Qy 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 2175 CCGCTCAAGGCCACCGACTTCGGCTCTCCGCTCTTCTCAAGGAGGGGAGCTGCTCAGG 2234
Qy 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
Db 2235 GACATCGTCGCGACGCGCTACTACATCGCGCGCGAGGTGCTCAAGAGGAAGTACGGCGCG 2294
Qy 206 GluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPro 225
Db 2295 GAGCCGACATCTGAGCGTCGGGCTCATGCTCTACATCTCTCCGCGCGGCTGCTCC 2354
Qy 226 PheTrpAla----- 228
Db 2355 TTCTGGGC-AGGTCCGATCCGTCGCTGTCCTAGACGATATACAGAACCCGACGATG 2413
Qy 229 -----GluThrGluSerGlyIlePheArgGln 237
Db 2414 GATTGGCTTCTCAGCCCTGTTCTTTCATCACAGAGAACGAGACGGCATCTTCACGCGC 2473
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAlaAla 257
Db 2474 ATCTCGGAGGGAGCTTGACTCTCCAGCGAGCATGGCCACACATCTCGCCGGGAGCC 2533
Qy 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db 2534 AAGGATCTCGTCAAGAAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGGCTTCAG 2593
Qy 278 AlaLeuCys----- 280
Db 2594 GTCCTCAG-TAAGTACCAGATCGTGTGTCATACACTCATATGAATTTGTATGTTTCAT 2652
Qy 281 -----HisProTyrIleValAspGln 288
Db 2653 GAGCAACGATCGAGCGGATTTGGTGAACCTGTAGATCACCCTCGATCAAGAAGACGGA 2712
Qy 289 AlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGln 308
Db 2713 GACGCGCTGACACGCGCTTGACAACGTTGTTCTCGACAGGCTCAAGCAGTTCAGGCGC 2772
Qy 309 MetAsnLysIleLysMetAlaLeuArgVal----- 319
Db 2773 ATGAACCATGTTCAAGAAGCAGCATTCAGGCTACATTATCTGATAAAAGCTCCACAAATA 2832
Qy 319 ----- 319
Db 2833 CAACCTCTGAAGACAGCAATGCTTACACGCGAGAAATTTTCATTATATAATGCTCTTGATG 2892
Qy 320 -----IleAlaGluArgLeuSerGluGluIleGlyLeuLysGlu 334
Db 2893 ACATAATGTTAGATCATAGCTGGTGGCTATCCGAGAGGAGATCACAGGCTGAAGGAG 2952
Qy 335 LeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAla 354
Db 2953 ATGTTCAAGAACATTGCAAGAGATAACAGCGGACCATTTACCTTCGACGAGCTCAACAC 3012
Qy 355 GlyLeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAla 374
Db 3013 GGGTTGGCAAGCAGCGGCCCAAGCTGTCCAGACAGCGAATGGAGAACTAATGGAGCA 3072
Qy 374 ----- 374
Db 3073 GTGAGTTTTCAGAGTACAATCTTAAAAAAGGAATTGTGATTTCTTTTCAAAATGAAGAAG 3132
Qy 375 -----AlaAspIleAspAsnSe 380
Db 3133 TAATCTGAAACATCCCTGCTGAATGCTTTATACATTTCCAGGCTGACGCTCAGCGGCAA 3192
Qy 380 rGlyThrIleAspTyrGlyGluPheLeuAlaIleThrLeuHisMetAsnLysMetGluAr 400
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Db 3193 CGGGTTAAATTCAGTACACGAATTCGTCACCGCAACAGTGCATATGAACAACTGGATAG 3252
Qy 400 gGluGluIleLeuValAlaIlePheSerAspPheAspLysAspGlySerGly----- 417
Db 3253 AGAAGACACCTTTACACAGCATTCACAGATTCAGATATTCGACACAGGACACAGCGG-GTAAGTTG 3311
Qy 417 ----- 417
Db 3312 AACGTTAAATGATACAGCTGGTACCTGGAATTTCTGGACAACACATATCATAAACAGGACAC 3371
Qy 418 -----TyrIleThrIleAspGluLeuGlnSerAlaCysTh 429
Db 3372 ATATATAATTCGTTTATCTCACAGGTACATTTACTTAAAGAGAGCTTCAGCACGCTTGAA 3431
Qy 429 rGluPheGlyLeuCysAspThr---ProLeuAspAspMetIleLysGluIleAspLeuAs 448
Db 3432 GGAGCAAGGGTTGTATGACGCCGCTAATAAATCAAGACATCATCTCCGATGCCGACTCTGA 3491
Qy 448 pAsn----- 449
Db 3492 CAA-TGTAAGGAACAAACATTTTAAATTTTCAGCCGACAAACTTAAACTATAGAAACAC 3550
Qy 449 ----- 449
Db 3551 ATCATGATATCAAAATTTTGAGTGGCGGTGCTACAGAAATAGAACCCAGTACACAAAT 3610
Qy 449 ----- 449
Db 3611 GACTAACTTGTCTGATGTTGTTGTTCTCTGTAACCTGAACATTTGTGTTCTTAGTTCTTA 3670
Qy 450 -----AspGlyLysIleAspPheSe 456
Db 3671 TTGTTAAACCAAGACTTAAATTCATTTTGCATGTCAGGATGGAAGGATAGATTATTC 3730
Qy 456 rGluPheThrAlaMetMetArgLysGly 465
Db 3731 AGAGTTTGTGCGATGATGAGGAAGGG 3758

RESULT 13
US-09-347-801-3
; Sequence 3, Application US/09347801
; Patent No. 6262345
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Lee, Jian Ming
; TITLE OF INVENTION: Plant Protein Kinases
; FILE REFERENCE: BB-1171
; CURRENT APPLICATION NUMBER: US/09/347,801
; EARLIER FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,438
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 3
; LENGTH: 2374
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-347-801-3

Alignment Scores:
Pred. No.: 3,03e-82 Length: 2374
Score: 831.00 Matches: 187
Percent Similarity: 58.30% Conservative: 94
Best Local Similarity: 38.80% Mismatches: 165
Query Match: 32.05% Indels: 36
DB: Gaps: 12

US-09-848-806-1 (1-495) x US-09-347-801-3 (1-2374)
Qy 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGlu 45
Db 708 TACGAGCTCGGAGAGGAGGTGGGAGGGCCACTTCGGACACACT-----TGCTCCGCC 761
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QY 46 LysSerThrSerAlaAsnTyr-----AlaCysLysSerIleProLysArg 60  
Db 762 GTCGTCAGAAAGGGCGAGTACAAAGGACACACGCGTCAAGATCATCGCAAGCT 821  
QY 61 LysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisHis 80  
Db 822 AAGATGACAAACGGCAATATCCATTGAGGATGTTGCTAGAGAAAGTAAATAATTTTGAGAGCG 881  
QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100  
Db 882 TTATCAGGGCACAAATAATCTCGTCAAAATCTATGATGCGATGTGAGGATGCGCTCAATGTC 941  
QY 101 HisIleValMetGluValCysGluGlyGluLeuPheAspArgIleValSerLys---- 119  
Db 942 TACATTGTCATGGAATATTATGTGAGGAGGAGAAATTTGCTAGACAGAAATATTAGCCAGGCG 1001  
QY 120 GlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGlu 139  
Db 1002 GGGATATACAGAGAGAGATGCCAAGCGATTTGTTACAGATTTTGAGCGTAGTAGCC 1061  
QY 140 AlaCysHisSerLeuGlyValMetHisArgAspLeuLeuPheProGluAsnPheLeuPheAsp 159  
Db 1062 TTCTGTCATCTTCAGGGGTAGTCATGCTGATGTTGAAGCCAGAGAAATTTCTTTTTCACA 1121  
QY 160 SerProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLys 179  
Db 1122 ACCAGGGATGAAATGCTCCCAAGTTGATTTGATTTGTTGCTCTCTGATTTTCATTAGA 1181  
QY 180 ProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeu 199  
Db 1182 CCAGATGAAGCGCTTAATGATATTGTTGAAGTGCATATTATGTTGCCCCAGAGGTTTTPA 1241  
QY 200 LysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeu 219  
Db 1242 CACAGATCATATAGTATGGAACACACATTTGAGTATAGTGTCTATACGTCATCTG 1301  
QY 220 LeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeu 239  
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QY 240 GlnGlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaLysAsp 259  
Db 1362 AGAGCTGATCCCACTTTGATGATTCACCGTGGCTACAGTATCAGCTGAAGCTAAGGAT 1421  
QY 260 LeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeu 279  
Db 1422 TTTGGAAGAGATTCTGAACAAAGATTACCGCAAGAAATGACCGCTGTTCAAGCACTG 1481  
QY 280 CysHisProTrpIleValAspGluGlnAlaProAspLysProLeuAspProAlaVal 299  
Db 1482 ACTCATCTCTGGTTCGGAGATGAACAAAGG-----CAGATCCCGCTGCACATCTCATC 1535  
QY 300 LeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysMetAlaLeuArgVal 319  
Db 1536 TTCAGATTAAATTAAGCAATACCTCCGCGTACACCTCTTAAACGGTTGGCATTTAAAGCA 1595  
QY 320 IleAlaGluArgLysSerGluGluIleGlyLeuLysGluLeuPheLysMetIle 339  
Db 1596 CTATCCAAGGCTTTAAGGGAAGATGAATTTTGTATCTCAAACTGCAGCTTTAAACTGCTC 1655  
QY 340 AspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgVal 359  
Db 1656 GAA---CCTAGAGATGGGTTTGTATCACTTGACAACTTTTCGACCGGCCTAACCGGATAT 1712  
QY 360 GlySerGluLeuMet---GluSerGluIleLysSerLeuMetAspAlaAlaAspIleAsp 378  
Db 1713 TTAAGTATGATATGAAGAAATCGAGGTTTCTGAAATTTTTCATGCGTTCGACCACTT 1772  
QY 379 AsnSerGlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeu-----HisMet 395  
Db 1773 GCATACAGAAATGCGATTGGAAGAGTTCTGTGCCGAGCAATCAGTCCTTACCAGCTT 1832

QY 396 AsnLysMetGluArg---GluGluIleLeuValAlaAlaPheSerAspPheAspLysAsp 414  
Db 1833 GAGGCACCTGGAAGGTGGGAGGAGATTCCTGGAAACAGCTTTCCAGCAATTTGACAGAG 1892  
QY 415 GlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCys 434  
Db 1893 GCGAACCCGAGTCATATCATGCTTGGAGAAATTA-----GCACAGGAATTTAAATCTTGT 1943  
QY 435 AspThrPro-----LeuAspAspMetIleLysGluIleAspLeuAspAsnAspGly 451  
Db 1944 CCAATCTTACTTCCATGCTTCAAGACTGGATCAGAAAA-----TCCGATGGC 1991  
QY 452 LysIleAspPheSerGluPheThrAlaMetMet----- 462  
Db 1992 AAGCTAAACTTCTCGGGTTTACCAAAATTTTACATGGTGTCAATAAGGGGCTCAAT 2051  
QY 463 ---ArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsn 481  
Db 2052 ACAAGACGGCATTAAGCGATTTGCAAAAGAAATGATTTCTTCTTCTTAATTTTAAA 2111  
QY 482 IleAla 483  
Db 2112 GCCGCT 2117  
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US-08-464-164-1  
; Sequence 1, Application US/08464164  
; Patent No. 5614195  
; GENERAL INFORMATION:  
; APPLICANT: Tomley, Fiona M.  
; APPLICANT: Dunn, Paul P. J.  
; APPLICANT: Bumstead, Janene M.  
; APPLICANT: Vermeulen, Arno N.  
; TITLE OF INVENTION: Coccidiosis poultry vaccine  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Akzo No. 5614195el Patent Department  
; STREET: 1300 Piccard Drive, Suite 206  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: U.S.A.  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/464,164  
; FILING DATE: June 2, 1995  
; CLASSIFICATION: 435,  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Gormley, Mary E.  
; REGISTRATION NUMBER: 34,409  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 258-5200  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1400 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: C-terminal  
; ORIGINAL SOURCE:  
; ORGANISM: Eimeria maxima  
; STRAIN: Houghton  
; DEVELOPMENTAL STAGE: sporozoite  
; IMMEDIATE SOURCE:  
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII  
; CLONE: Em70-1





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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Eimeria maxima
; STRAIN: Houghton
; DEVELOPMENTAL STAGE: sporozoite
; IMMEDIATE SOURCE:
; LIBRARY: sporozoite cDNA cloned in Lambda ZAPII
; CLONE: Em70-1
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1368
; US-08-338-057-1

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Alignment Scores:
Pred. No.: 5,45e-76 Length: 1400
Score: 771.50 Matches: 165
Percent Similarity: 57.81% Conservative: 94
Best Local Similarity: 36.83% Mismatches: 162
Query Match: 29.75% Indels: 27
DB: 1 Gaps: 8

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US-09-848-806-1 (1-495) x US-08-338-057-1 (1-1400)

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QY 58 ProLysArgLysLeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIle 77
DB 79 TCTAAACGTCAGTAAACAGAGACAGATATAAGAAATTTATTATAAAGAGTTGAATTA 138
QY 78 MetHisHisLeuSerGluHisProAsnValAlaArgIleLysGlyThrTyrGluAspSer 97
DB 139 TTAACAGAAATTA---GATCATCTTAATATCATGAAATTTATGAAATCTTTGAGGATAAA 195
QY 98 ValPheValHisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleVal 117
DB 196 GGATACTTTTATCTGTTACAGAAGTATATACAGGAGGAGAGATTTATTCATGAAATATT 255
QY 118 SerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyVal 137
DB 256 AATCGAAAAAGATTTCAGCGAGCGGATCGTAGCTCGTATAGTACGTCAGGTTCTATCGGCT 315
QY 138 ValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeu 157
DB 316 ATAAATTATATGATCGTAAATAAATAGTTTCATAGAGATTTAAAGCCAGAGAAATTTATTA 375
QY 158 PheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPhe 177
DB 376 TTAGAGATAAAAAAAGATGCAATATACGAATTTATGATTTGGGTTATCTACACAT 435
QY 178 TyrLysProGlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGlu 197
DB 436 TTTGAGCCCCAAAAAATGAAGATATAAATCGGACCGCGTACTACATTCGCCCTGAG 495
QY 198 ValLeuLysLysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyr 217
DB 496 GTGCTGCACGGAACATACATGAGAAATCGCAGCGTCTGGTCTACGGGTGTTATCCTCTAT 555
QY 218 IleLeuLeuSerGlyValProProPheTrpAlaGluThrGluSerGlyIlePheArgGln 237
DB 556 ATCCTTCTCTCTGGTTGTCCTCAATTAACGGAGCAATGAATTTCAAATTCATAAGAAA 615
QY 238 IleLeuGlnGlyLysLeuAspPheLysSerAspProTrpProThrIleSerGluAla 257
DB 616 GTCGAGAAAGGAAATTCACCTTCGATTTTACCACAGTCGCGTAAGGTTAGCGAGCAGCA 675
QY 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277

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DB 676 AAAGATTTAATTAGGAAGATGTTAGCATATGTATCCCTCAATGCGTATATCAGCAAAAGAT 735
QY 278 AlaLeuCysHisProTrpIle-----ValAspGluGlnAlaAlaProAspLys 293
DB 736 GCATTAGATCATCCATGGATAAAAAGTACAGATGTTTACTGCTAAGGATAGTATTAAATCTT 795
QY 294 ProLeuAspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLys 313
DB 796 CCTTCTCTTGAGAGTACTACTTAATATCAGGCAGTTCAGGGGTACACAGAGCTTGCT 855
QY 314 LysMetAlaLeuArgValIleAlaGluArgLeu---SerGluGluGluIleGlyGlyLeu 332
DB 856 GCTGCTGCTCTGCTGTACATGGGAGTAAATTAACAACAATCAGGAGACAGACGAATTG 915
QY 333 LysGluLeuPheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeu 352
DB 916 AATAAAATCTTCAGGAAGATGGATAAGAACGGAGACGCACTCGATATAACAAGAATTA 975
QY 353 LysAlaGly-----LeuLysArgValGlySerGluLeu----- 363
DB 976 ATGAGGGTTATCTTGAATTAATGAAGCTAAAGGAGAGAGATGTTTCTGTATTAGACAAG 1035
QY 364 -----MetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGly 381
DB 1036 AGTGCAATTGAGACAGAGAGTGAACAAGTCTCTTGAGGCTGTAGACTTCGATAAGAATGGA 1095
QY 382 ThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGlu 401
DB 1096 TTTATTGAATATTCAGAAATTCGTGACGGTGGCAATGGATAGAGAACTCTGTTTATCAAGA 1155
QY 402 GluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThrIle 421
DB 1156 CAAAGACTTTGAAAGAGCATTCAGATGTTTCGACTCGATGGATCAGGAAAAATCTCTCTC 1215
QY 422 AspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp--- 440
DB 1216 TCTGAATTA-----GCTACTATATTTGGTGTAAAGCAG-----TTAGACTCGGAG 1260
QY 441 -----MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSer 456
DB 1261 GCATGGCGTCGGGTATTAGCAGAAAGTTGATCGAAATATGACGGAGAGTTGACTTTGAG 1320
QY 457 GluPheThrAlaMetMetArgLys 464
DB 1321 GAATTTACAGCAATGCTTCTTAAA 1344

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Search completed: November 28, 2003, 13:22:43  
Job time : 138 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 28, 2003, 12:32:03 ; Search time 1177 Seconds  
(without alignments)  
1385.617 Million cell updates/sec

Title: US-09-848-806-1

Perfect score: 2593

Sequence: 1 METKPNRPNSNTVLPYQTP.....KNLNFNIADAFGVGDEKSD 495

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2190069 seqs, 1647345023 residues

Total number of hits satisfying chosen parameters: 4380138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters: -MODEL=frame+ p2n.model -DEV=xlh  
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-DB=Published Applications NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
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-NCPU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100  
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Database : Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 14: /cgn2\_6/ptodata/2/pubpna/US10B\_PUBCOMB.seq:\*
- 15: /cgn2\_6/ptodata/2/pubpna/US10C\_NEW\_PUB.seq:\*
- 16: /cgn2\_6/ptodata/2/pubpna/US10C\_PUBCOMB.seq:\*
- 17: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	ID	Description
1	2593	100.0	1747	12 US-10-289-172-2

Alignment Scores: 1.73e-287 Length: 1747  
Pred. No.: 2593.00 Matches: 495  
Score: 100.00% Conservative: 0

ALIGNMENTS

RESULT 1

US-10-289-172-2  
; Sequence 2, Application US/10289172  
; Publication No. US20030154504A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: Calcium Dependent Protein Kinase  
; FILE REFERENCE: 00786/183002  
; CURRENT APPLICATION NUMBER: US/10/289,172  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 1747  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-289-172-2

2	2593	100.0	1747	12	US-09-848-806-2	Sequence 2, Appli
3	2577	99.4	1488	10	US-09-938-842A-704	Sequence 704, App
4	2458	94.8	1657	12	US-10-289-172-4	Sequence 4, Appli
5	2458	94.8	1657	12	US-09-848-806-4	Sequence 4, Appli
6	1844.5	71.1	1473	10	US-09-938-842A-786	Sequence 786, App
7	1731	66.8	1635	10	US-09-938-842A-2344	Sequence 2344, Ap
8	1724	66.5	1833	10	US-09-938-842A-2334	Sequence 2334, Ap
9	1509.5	58.2	2230	9	US-09-828-313-26	Sequence 26, Appl
10	1381	53.3	1638	10	US-09-938-842A-1859	Sequence 1859, Ap
11	1313.5	50.7	1602	10	US-09-938-842A-2304	Sequence 2304, Ap
12	1277.5	49.3	1349	11	US-09-988-462-20	Sequence 20, Appl
13	1159.5	44.7	4162	11	US-09-988-462-26	Sequence 26, Appl
14	857.5	33.1	1387	9	US-09-828-313-13	Sequence 13, Appl
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16	831	32.0	2374	10	US-09-854-731-3	Sequence 3, Appli
17	803.5	31.0	1800	10	US-09-938-842A-1063	Sequence 1063, Ap
18	726	28.0	455	9	US-09-770-444-571	Sequence 571, App
19	687	26.5	955	9	US-09-770-445-326	Sequence 326, App
20	591	22.8	1500	12	US-10-354-358-87	Sequence 87, Appl
21	591	22.8	1500	12	US-10-393-892-1	Sequence 1, Appli
22	591	22.8	1500	12	US-10-394-382-1	Sequence 1, Appli
23	587.5	22.7	1480	12	US-10-204-041-9	Sequence 9, Appli
24	581.5	22.4	5637	10	US-09-917-800A-1537	Sequence 1537, Ap
25	578.5	22.3	1740	12	US-10-320-351-14	Sequence 14, Appl
26	578.5	22.3	1740	12	US-10-320-351-14	Sequence 14, Appl
27	578	22.3	1458	12	US-09-735-138-5	Sequence 5, Appli
28	569.5	22.0	1825	12	US-10-116-275-321	Sequence 321, App
29	568.5	21.9	2218	12	US-09-820-790-1	Sequence 1, Appli
30	565	21.8	1551	9	US-09-925-299-210	Sequence 210, App
31	565	21.8	1551	11	US-09-925-299-210	Sequence 210, App
32	564.5	21.8	1578	9	US-09-835-788A-6	Sequence 6, Appli
33	564.5	21.8	1578	12	US-10-175-042-6	Sequence 6, Appli
34	561.5	21.7	1733	14	US-10-037-270-526	Sequence 526, App
35	558.5	21.5	1694	12	US-10-355-975-3	Sequence 3, Appli
36	558.5	21.5	3705	13	US-10-044-090-227	Sequence 227, App
37	557.5	21.5	1772	14	US-10-024-036B-1	Sequence 1, Appli
38	554	21.4	1074	14	US-10-024-036B-3	Sequence 3, Appli
39	543	20.9	1383	11	US-09-935-464-2	Sequence 2, Appli
40	543	20.9	1383	14	US-10-125-835-2	Sequence 2, Appli
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42	543	20.9	2061	13	US-10-125-835-4	Sequence 4, Appli
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-848-806-1 (1-495) x US-10-289-172-2 (1-1747)

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QY 21 ArgLeuArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyThrThr 40
DB 127 CGATTAAAGAGATCATTTACCTTCTGGGAAAAAAGCTAGGCCCAAGCCCAATTTGGAACAACC 186
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DB 187 TATCTCTGCACAGAGAAATCAACCTCCGCTAAATACGCCCTGCAATTCGATCCCGAAGCGA 246
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DB 247 AAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGGCTGAGATTTCAGATCATGCATCAT 306
QY 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
DB 307 CTCCTCGACATCCAAATGTTGTAGGATCAAAAGGACTTATGAAGATTTCGTTGTTGTT 366
QY 101 HisIleValMetGluValCysGluGlyGlyLeuPheAspArgIleValSerLysGly 120
DB 367 CATATTGTTATGAGGTTTGTGAAGGTGTGAGCTTTTGAACGATTGTTTCTAAAGGT 426
QY 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
DB 427 CATTTTAGTGAGCGTGAAGCTGTCAAGCTTATTAGACGATTCTTGGTGTGTTGAGGCT 486
QY 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProLysPheLeuPheAspSer 160
DB 487 TGTTCATCTCTGTTGTTATGCTATGATAGATCTCAAAACCTGAGAATTTCTTGTGTAGT 546
QY 161 ProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180
DB 547 CCTAAGATGATGCTAAGCTTAAGGTACGATTTTGGTTGTCTCTCTATAAGCCA 606
QY 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200
DB 607 GGACAATATTTATGACGTAGTTGGAAGTCCGTACTATGTTGCACACAGGTGCTAAAG 666
QY 201 LysCysTyrGlyProGluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeu 220
DB 667 AAATGTTATGGACCTGAAATAGATGTGTGGAGTGTGTTATCTCTACATTTTACTC 726
QY 221 SerGlyValProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
DB 727 AGCGGTGTTCTCCCTTCTGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCAA 786
QY 241 GlyLysLeuAspPheLysSerAspProTyrProThrIleSerGluAlaLysAspLeu 260
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QY 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
DB 847 ATCTATAAATGCTCGAAGAGGAGCCCAAGAAACCGCATTTCTGCTCATGAAGCCCTGTGT 906
QY 281 HisProTyrIleValAspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeu 300
DB 907 CACCCATGGATTGTTCGATGAACAAGCAGCAGCAGACAGCCCTTTCATCCACAGTCTTA 966
QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
DB 967 TCTCGCTAAAGCAGTTTCTCAAAATGAATAGATTAAAGAAATGGCATTACCGGTAAAT 1026
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DB 1387 ATGATCAAGGAGATTGATCTTGACAATGACGGGAGATCGATTTCTCGGAGTTTACAGCA 1446
QY 461 MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe 480
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QY 481 AsnIleAlaAspAlaPheGlyValAspGlyGluLysSerAspAsp 495
DB 1507 AACATGCTGATGCTTTTGGAGTTGATGGTGGAATAATCTGATGAC 1551
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## RESULT 2

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US-09-848-806-2
; Sequence 2, Application US/09848806
; Publication No. US20030167516A1
; GENERAL INFORMATION:
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; APPLICANT: Sheen, Jen
; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; TITLE OF INVENTION: Polypeptides as Regulators of Plant Disease Resistance
; FILE REFERENCE: 00786/389002
; CURRENT APPLICATION NUMBER: US/09/848,806
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1747
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-848-806-2
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Score: 2593.00 Matches: 495
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
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US-09-848-806-1 (1-495) x US-09-848-806-2 (1-1747)
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DB 67 ATGAGACGAGCGAAGCAAAACCTAGACGTCCTTCAAAACACAGTTCTACCATATCAAAACCA 126
QY 21 ArgLeuArgAspHisTyrIleLeuLeuGlyLysLysLeuGlyGlnGlyPheGlyThrThr 40
DB 127 CGATTAAAGAGATCATTTACCTTCTGGGAAAAAAGCTAGGCCCAAGGCCAATTTGGAACAACC 186
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Qy 81 LeuSerGluHisProAsnValValAArgLysGlyThrTyrGluAspSerValPheVal 100
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Qy 101 HisIleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120
Db 367 CATATTGTATGAGGTGTGTGAAGGTGGTGAGCTTTTTCATCGGATGTTCCTAAAGGT 426
Qy 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140
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Qy 221 SerGlyValProPheProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240
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Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280
Db 847 ATCTATAAAATGCTCGAAAGGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCTTGTGT 906
Qy 281 HisProTyrIleValAspGluGlnAlaProAspLysProLeuAspProAlaValLeu 300
Db 907 CACCATGATTTGTCATGAACAAGCAGCAGCAGCAAGCCCTCTTGATCCAGAGTCTTA 966
Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320
Db 967 TCTCGCTAAAGCAGTTTTCTCAAAATGAATAAGATTAAAGAAATGGCATTACGGTAAAT 1026
Qy 321 AlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
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Qy 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360
Db 1087 ACAGACAACAGCGGAACGATTTACTTTTGAAGAGCTCAAGCCGGTTTGAAGAGAGTCGA 1146
Qy 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
Db 1147 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGGATCGCGCTGATATCGACAACAGT 1206
Qy 381 GlyThrIleAspTyrGlyPheLeuAlaThrLeuHisMetAsnLysMetGluArg 400
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Db 1327 ATCGATGAGCTTCAGTCAGCTTCGCACAGAGTTTGGTCTATGTGATACACCTCTGGAGC 1386
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Db 1387 ATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTTCTCGGAGTTTACAGCA 1446
Qy 461 MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe 480
Db 1447 ATGATGAGGAAGGAGATGGAGTTGGGAGAGCAGAACCATGATGAAGAACTTGAACATTC 1506
Qy 481 AsnIleAlaAspAlaPheGlyValAspGlyGluLysSerAspAsp 495
Db 1507 AACATTGCTGATGCTTTTGGAGTTGATGGTGAAGAAATCTGATGAC 1551

RESULT 3
US-09-938-842A-704
; Sequence 704, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPT300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 704
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-704

Alignment Scores:
Pred. No.: 9,388-286 Length: 1488
Score: 2577.00 Matches: 493
Percent Similarity: 99.60% Conservative: 0
Best Local Similarity: 99.60% Mismatches: 2
Query Match: 99.38% Indels: 0
DB: 10 Gaps: 0

US-09-848-806-1 (1-495) x US-09-938-842A-704 (1-1488)

Qy 1 MetGluThrLysProAsnProArgProSerAsnThrValLeuProTyrGlnThrPro 20
Db 1 ATGGAGACGAGCCAAACCTTAGAGCTCTTCAACACACAGTTCTACCATATCAACACCA 60
Qy 21 ArgLeuAArgAspHisTyrLeuLeuGlyLysLysLeuGlyGlnPheGlyThrThr 40
Db 61 CGATTAAAGAGATCATTTACCTTCTGGGAAAAAGCTAGGCCAAGGCCAATTTGGAAACACC 120
Qy 41 TyrLeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArg 60
Db 121 TATCTCTGCACAGAGAAATCAACTCCGCTAATTACGCTGCAAAATCGAATCCCGAAGCGA 180
Qy 61 LysLeuValCysArgGluAspTyrGluAspValTyrArgGluIleGlnIleMetHisHis 80
Db 181 AAGCTCGTGTGTCGCGAGGATTACGAAGATGTATGGCGTGAGATTTCAGATCATGCATCAT 240
Qy 81 LeuSerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheVal 100
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Db 241 CTCTCTGAGCATCCAAATGTTGTTAGGATCAAGGGACTTATGAAGATTTCGGTGTGTTT 300  
Qy 101 HisLeValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGly 120  
Db 301 CATATTGTTATGGAGGTTGTGAAGGTGGTGAAGCTTTTGTGATCGGATTGTTCTAAAGGT 360  
Qy 121 HisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAla 140  
Db 361 CATTTTATGAGCGTGAAGCTGTCAAGCTTATTAAAGACGATTCTTTGGTGTGTTGAGGCT 420  
Qy 141 CysHisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSer 160  
Db 421 TGTCAATCTCTGTTGTTATGCATAGAGATCTCAAACTCGAGAATTTCTTGTGATAGT 480  
Qy 161 ProLysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysPro 180  
Db 481 CCTAAAGATGATGCTAAAGCTTAAGGCTACCGATTGTTGTTGTTCTCTCTATAAGCCA 540  
Qy 181 GlyGlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLys 200  
Db 541 GGACATATTTATATGACGTAGTTGGAAGTCCGTACTATGTTGCACACAGAGGTCTAAAG 600  
Qy 201 LysCysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeu 220  
Db 601 AAATGTTATGACCTGAAATAGATGCTGTGGAGTCTGGTGTATCTCTACATTTTACTC 660  
Qy 221 SerGlyValProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGln 240  
Db 661 AGCGGTGTTCTCCCTCTCGGGCAGAGACTGAGTCTGGAATCTTTAGACAGATATTGCA 720  
Qy 241 GlyLysLeuAspPheLysSerAspProTrpThrIleSerGluAlaAlaLysAspLeu 260  
Db 721 GGGAGCTTAGATTTCAAAATCTGACCCGTGGCTACTATCTCAGAAGCTGCTAAAGATTG 780  
Qy 261 IleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCys 280  
Db 781 ATCTATAAAATGCTCGAAAGAGAGCCCAAGAAACGCAATTTCTGCTCATGAAGCCTTGT 840  
Qy 281 HisProTrpIleValAspGluAlaAlaProAspLysProLeuAspProAlaValLeu 300  
Db 841 CACCATGGAATGTCGATGAACAAGCAGCAGCACCAAGCCCTCTGTATCCAGCAGCTTA 900  
Qy 301 SerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIle 320  
Db 901 TCTCGTCTAAAGCAGTTTCTCAATGAATTAAGATTAAAGAAATGGCATTAACGGGTAA 960  
Qy 321 AlaGluArgLeuSerGluGluIleGlyLeuLysGluLeuPheLysMetIleAsp 340  
Db 961 GCTGAGAGACTTTCAGAGGAAGAAATTTGGAGGTCTGAAGGAATTTGTTCAAGATCATAG 1020  
Qy 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGly 360  
Db 1021 ACAGACAACAGCGGACGATTACTCTTTGAAGAGCTCAAGCGGTTTGAAGAGAGTCGA 1080  
Qy 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380  
Db 1081 TCTGAACCTGATGGAATCAGAAATCAAGTCTCTCATGATGCGGTGATATCGACAACAGT 1140  
Qy 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrIleLysMetAsnLysMetGluArg 400  
Db 1141 GGTACAATAGACTACGGAGAATTCCTAGCAGCAACCTTACACATGAACAAGATGGAGAGA 1200  
Qy 401 GluGluIleLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420  
Db 1201 GAGAGAAATCTGGTGGCTGCATTTCTGTAATTTGACAAAGACGGAACGGGTATATCACC 1260  
Qy 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440  
Db 1261 ATCGATGAGCTTCAGTCAGCTTGACAGAGTTTGGTCTATGTGATACACCTCTGGACGAC 1320  
Qy 441 MetIleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460  
Db 1321 ATGATCAAGGAGATTGATCTTGACAATGACGGGAAGATCGATTCTTCGGAGTTTACAGCA 1380

Qy 461 MetMetArgLysGlyAspGlyValIleYargSerArgThrMetMetLysAsnLeuAsnPhe 480  
Db 1381 ATGATGAGAAAGAGATGGAGTTGGGAGAAAGCAGAACCATGATGAAGAACTTGAAC TTC 1440  
Qy 481 AsnIleAlaAspAlaPheGlyValAspGlyGluLysSerAspAsp 495  
Db 1441 AACATTGCTGATGCTTTTGGAGTTTGAATGGTGAATAAATCTGATGAC 1485  
RESULT 4  
US-10-289-172-4  
; Sequence 4, Application US/10289172  
; Publication No. US20030154504A1  
; GENERAL INFORMATION:  
; APPLICANT: Sheen, Jen  
; TITLE OF INVENTION: Calcium Dependent Protein Kinase  
; FILE REFERENCE: Polypeptides as Regulators of Plant Disease Resistance  
; CURRENT APPLICATION NUMBER: US/10/289,172  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/201,925  
; FILING DATE: 2000-05-05  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 1657  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-289-172-4  
Alignment Scores:  
Pred. No.: 5,15e-272 Length: 1657  
Score: 2458.00 Matches: 470  
Percent Similarity: 96.57% Conservative: 9  
Best Local Similarity: 94.76% Mismatches: 13  
Query Match: 94.79% Indels: 4  
Gaps: 12  
US-09-848-806-1 (1-495) x US-10-289-172-4 (1-1657)  
Qy 4 LysProAsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArg 23  
Db 7 AAACCAACCTTAGAGACCTCAACAGTGTCTTCATACAGAACACCAAGATTAA 66  
Qy 24 AspHisTyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCys 43  
Db 67 GATCAGTATCTCTCGGCAAAAGCTAGGCCAACATTTGGACCAACCTATCTCTGT 126  
Qy 44 ThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuVal 63  
Db 127 ACAGAGAAATCATCATCAGCTAATACGCTTGCAAAATCAATCCCAAAACGTAAGCTTGT 186  
Qy 64 CysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGlu 83  
Db 187 TGTGCGTAAGACTACGAGATGTATGCGTGAGATTGAGATCATGATCATCTCTCTGAG 246  
Qy 84 HisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleVal 103  
Db 247 CATCTAATGTTGTTAGAAATCAAGGGTACTTATGAGACTCTGTTTTTGTTCACATTGTT 306  
Qy 104 MetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer 123  
Db 307 ATGGAAGTTTGTGAAGGTGGTGGCTTTTGTGTCGGATTGTTCTAAAGGGTGTGTAGT 366  
Qy 124 GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer 143  
Db 367 GAACGTGAAGCTCTAAGTTGATTAAAGCTATTCTTGGTGTGTTGAGGCTGTGCTATCT 426  
Qy 144 LeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp 163  
Db 427 CTTGGTGTATGATAGAGATCTTAAGCCTGAGAAATTTCTTTGTTGATAGTCCAGTGAT 486  
Qy 164 AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyr 183

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487 GATGCTAAGCTTAAAGCTACAGACTTGGTTGCTGCTCTTACAAAGCAGGCAGTAT 546
QY
184 LeuTyAspValValGlySerProTyTyTyValAlaProGluValLeuLysCysTyTy 203
Db
547 CTGTATGATGATGTTGGAAGTCGGTATATGTTGACACCTGAGGTTCTGAAGAATGTTAT 606
QY
204 GlyProGluLeuAspValTrpSerAlaGlyValIleLeuTyTyIleLeuLeuSerGlyVal 223
Db
607 GGACACAGATAGACGCTGGAGCGCGTGTATCTTGTACATCTTACTAAGTGGGGT 666
QY
224 ProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleGluGlyLysLeu 243
Db
667 CTTCTCTTTTGGCGAAGAACCGAGTCAGGAATCTTTAGGCAGATATTGCAAGGAAGATA 726
QY
244 AspPheLysSerAspProTrpProThrIleSerGluAlaAlaLysAspLeuIleTyLys 263
Db
727 GATTTTAATCTGATCCGTGGCTACTATCTCAGAGGTGCTTAAGATTGATTACAAA 786
QY
264 MetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTrp 283
Db
787 ATGCTCGATAGGAGGCCCAAGAAACGTAATTTCTGCACATGAAGCAATGTGTACCCCTGG 846
QY
284 IleValAspGluClnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeu 303
Db
847 ATGTTGATGAACATCTCTGCACAGACAAAGCCCTCTCGACCCAGCAGTCTGTGCGACTT 906
QY
304 LysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArg 323
Db
907 AAGCAGTCTTCGCAATGAATAAATCAAGAAATGCGCTTACGAGTAATCGCGAGAGA 966
QY
324 LeuSerGluGluGluIleGlyLeuLysGluLeuPheLysMetIleAspThrAspAen 343
Db
967 CTTCTCGAGGAAGAGATTGGTGTCTGAAGGAATTTCTCAAAATGATAGATACAGACAAC 1026
QY
344 SerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySerGluLeu 363
Db
1027 AGTGGAAACAATCACCTTTCAAGAGCTTAAAGCAGGTCTAAAGAGAGTTGGATCTGAATTG 1086
QY
364 MetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAenSerGlyThrIle 383
Db
1087 ATGGAATCAGAATCAAGTCTCTTATGGATGCGCGGATATAGACAAAGTGGACAAATA 1146
QY
384 AspTyTyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluIle 403
Db
1147 GACTACGGTGAATTCCTAGCAGCGACATACATATATAACAAGATGGAGAGAGAAGAAC 1206
QY
404 LeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyTyIleThrIleAspGlu 423
Db
1207 TTGGTGGTGGCTTTTCATCTTTGATAAAGATGGTAGCGGTATATACCAATTGACGAG 1266
QY
424 LeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIleLys 443
Db
1267 CTTCAACAAGCCTGCACAGATTTGGTCTCTGTGACACTCTCTTGATCATATGATCAAA 1326
QY
444 GluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArg 463
Db
1327 GAGATTGATCTTGATAATACCGGAGATTTGATTTCTCAGAGTTTACTCTATGATGAAG 1386
QY
464 LysGlyAspGlyValGlyArgSerArgThrMetLysAsnLeuAsnPheAsnIleAla 483
Db
1387 AAAGAGATGGTGTGGGAGGAGCACTATGAGAAACAATCTGAACTTCAATATAGCT 1446
QY
484 AspAlaPheGlyValAspGly-----GluLysSerAspAsp 495
Db
1447 GAAGCTTTTGGAGTTTGAGGACACAAAGCAGCAGCTGCTAATCTGATGAT 1494
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## RESULT 5

US-09-848-806-4

; Sequence 4, Application US/0984806

; Publication No. US20030167516A1

; GENERAL INFORMATION:

; APPLICANT: Sheen, Jen

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; TITLE OF INVENTION: Calcium Dependent Protein Kinase
; FILE REFERENCE: Polypeptides as Regulators of Plant Disease Resistance
; CURRENT APPLICATION NUMBER: US/09/848,806
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: US 60/201,925
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 1657
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; US-09-848-806-4

Alignment Scores:
Pred. No.: 5,15e-272 Length: 1657
Score: 2458.00 Matches: 470
Percent Similarity: 96.57% Conservative: 9
Best Local Similarity: 94.76% Mismatches: 13
Query Match: 94.79% Indels: 4
DB: 12 Gaps: 1
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US-09-848-806-1 (1-495) x US-09-848-806-4 (1-1657)

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QY 4 LysProAsnProArgArgProSerAsnThrValLeuProTyTyGlnThrProArgLeuArg 23
Db 7 AAACCAACCCCTAGAGACCCCTCAACAGTGTCTCCATACGAACACCAAGATTNAGA 66
QY 24 AspHisTyTyLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrTyTyLeuCys 43
Db 67 GATCACTATCTCTCGCAAAAGCTAGCCCAAGGCCAATTTGGAACAACCTATCTCTGT 126
QY 44 ThrGluLysSerThrSerAlaAsnTyTyAlaCysLysSerIleProLysArgLysLeuVal 63
Db 127 ACAGAGAAATCATCATCTACGCTAATACGCTTGCATAATCAATCCCAAAACGTAAGCTTGA 186
QY 64 CysArgGluAspTyTyGluAspValTyTyArgGluIleGlnIleMethHisHisLeuSerGlu 83
Db 187 TGTCTGAGACATACGAAGATGTATGGCGTGAGATTGAGATCATGATCATCTCTCTGAG 246
QY 84 HisProAsnValValArgIleLysGlyTyTyTyTyGluAspSerValPheValHisIleVal 103
Db 247 CATCTCTAATGTTGTAGAAATCAAGGCTACTTATGAAGACTCTGTTTGTTCACATGTT 306
QY 104 MetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSer 123
Db 307 ATGGAAGTTTGTGAAGGTGGTGAGCTTTTGTATCGGATTTGTTCTAAAGGGTCTTTTAGT 366
QY 124 GluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSer 143
Db 367 GAACGTGAAGCTGCTAAGTTGATTGAAGACTATTCTTGGTGTGTGAGGCTTGTCTTCT 426
QY 144 LeuGlyValMethHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAsp 163
Db 427 CTTGGTGTATTGATCATAGAGATCTTAAGCCCTGAGAATTTCTTGTTCATAGTCCCGATG 486
QY 164 AspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyTyLysProGlyGlnTyTy 183
Db 487 GATGTAAGCTTAAAGCTACAGACTTTGGTGTGTTGCTCTCTTCTACAAAGCAGGCGAGTAT 546
QY 184 LeuTyAspValValGlySerProTyTyTyTyValAlaProGluValLeuLysCysTyTy 203
Db 547 CTGTATGATGATGTTGGAAGTCCGCTATTATGTTGACCTGAGGTTCTGAAGAAATGTTAT 606
QY 204 GlyProGluIleAspValTrpSerAlaGlyValIleLeuTyTyIleLeuLeuSerGlyVal 223
Db 607 GGACACAGATAGACGCTGTGGAGCCCGGTGTATCTTGTGTACATCTTACTAAGTGGGGT 666
QY 224 ProProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeu 243
Db 667 CCTCTCTTTTGGGCAAGAACCGAGTCAGGAATCTTTAGGCAGATATTGCAAGGAAGATA 726
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Db 829 CATCCGTTGGATTGCGATGAAGTTGCTCCAGATAAACTTTGGACTCGCGGTAGTG 898
QY 301 SerArgLeuLysGlnPheSerGlnMetAsnLysLleLysLysMetAlaLeuArgValIle 320
Db 889 TCCCGCTGAAGAGTTCTCTGCAATGAACAACCTTAAGAAGATGGCTTTACGAGTTATT 948
QY 321 AlaGluArgLeuSerGluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAsp 340
Db 949 GCAGAGAGACTATCTGAGGAAGAAATCGGTGGTCTCAAGAACTGTTTCAAAATGATAGAC 1008
QY 341 ThrAspAsnSerGlyThrIleThrPheGluGluLeuLysLaglyLeuLysArgValGly 360
Db 1009 ACAGATAAAAGTGGGACTATCAGCTTTGAAGAGTTAAAGATAGTAGATGAGACGTGTGGG 1068
QY 361 SerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSer 380
Db 1069 TCAGAGCTTATGAATCAGAGATCCAGAACTCTTGGCTGGGCTGATGTTGATGAGAGT 1128
QY 381 GlyThrIleAspTyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArg 400
Db 1129 GGAACAATGACTATGAGAGATTCTTAGCTGCAACAATCCACTTGAACAAGCTGGAGAGA 1188
QY 401 GluGluLeuValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrIleThr 420
Db 1189 GAGGAGAATCTAGTAGCTGCAATCTCTTCTTTGATAAGGATCCAAAGTGTATACACT 1248
QY 421 IleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAsp 440
Db 1249 ATCGAAGAGCTTCAACAGGCATCGAAGGAGTTTGGTATATAACGATTCATATCTTGATGA 1308
QY 441 MetIleGlyGluLeuAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla 460
Db 1309 ATGATCAAAAGACATTGATCAAGATAATGATGGACAAATAGACTATGAGAAATTTGGGCA 1368
QY 461 MetMetArgGlyAspGlyValGlyArgSer-----ArgThrMetMetLysAsn 477
Db 1369 ATGATGAGGAAGGAATGGCACTGGAGGAGGAGTTGGTCGGAGAACTATGAGGAACCTCT 1428
QY 478 LeuAsnPhe 480
Db 1429 CTCAACTTT 1437
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## RESULT 7

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US-09-938-842A-2344
; Sequence 2344, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIORITY FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 2344
; LENGTH: 1635
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2344
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Alignment Scores:  
Pred. No.: 1,658-188 Length: 1635  
Score: 1731.00 Matches: 328

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Percent Similarity: 81.88% Conservative: 65
Best Local Similarity: 68.33% Mismatches: 85
Query Match: 66.76% Indels: 2
DB: 10 Gaps: 2
US-09-848-806-1 (1-495) x US-09-938-842A-2344 (1-1635)
QY 6 AsnProArgArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25
Db 193 AACGTTGACAACTTCTTACTATGTTCTTGGTCAACAAGACTCTTAACATTCGTGATCTT 252
QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyrLeuCysThrGlu 45
Db 253 TACACGTTGAGTCGTAAAGTAGGACAAGGACAATTCGGGACAACGATTATTTGTTGCTACTGAT 312
QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65
Db 313 ATTGCCACAGGTTGACTATGCTTGTAAAGTCTATATCCAAAGAGGAAATATGATATCTAAA 372
QY 66 GluAspTyrGluAspValTyrArgGluIleGlnIleMetHisLysLeuSerGluHisPro 85
Db 373 GAAGATGTTGAGGATGTTAGGAGGAGATTCAGATTATGTCATCATTTAGCTGGTCACAAG 432
QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105
Db 433 AATATTGTTACTATTAAAGCAGCTTATGAGGATCCTTTGTTGTTTTCACATTGATGAGGAG 492
QY 106 ValCysGluGlyGlyGlyLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125
Db 493 CTTTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 552
QY 126 GluAlaValLysLeuLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145
Db 553 AAAGCTGCTGAGTTGACCAAGATCATTTGCGGTGTTGTTGAGCGGTGTCATTTCTTTGGT 612
QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAspAla 165
Db 613 GTTATGCATAGAGATTTAAAGCCTGAGAATTTCTTGTGTTAATAAGGATGATGATTTTC 672
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185
Db 673 TCTCTTAAAGGCCATTGATTTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 732
QY 186 AspValValGlySerProTyrTyrValAlaProGluValLeuLysLysCysTyrGlyPro 205
Db 733 GATGTTGTTGGAAGTCCATCATGTTGCTCTCTGAGGTTCTTCTAAACATTTATGTTCCA 792
QY 206 GluIleAspValTyrSerAlaGlyValIleLeuTyrIleLeuLeuSerGlyValProPro 225
Db 793 GAAAGCTGATGTGTGGACTGCTGGTGTATATCTATCTATCTTACTAAGTGGTGTCCCGCCT 852
QY 226 PheTyrAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe 245
Db 853 TTCTGGGAGAAACACACGCAAGGAATATTTGATGCTGTGTTGAAAGGATATATGACTTTT 912
QY 246 LysSerAspProTyrProThrIleSerGluAlaAlaLysAspLeuIleTyrLysMetLeu 265
Db 913 GATACAGACCCCGTGGCTGTCTATATCCGACATGCTTAAAGATCTGATCCGGAAGATGTTA 972
QY 266 GluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHisProTyrIleVal 285
Db 973 TGCTCTAGTCTCTTGAACGTTTGACTGCTCATGAAGTCTTGGTGCATCCATGGATCTGT 1032
QY 286 AspGluGlnAlaAlaProAspLysProLeuAspProAlaValLeuSerArgLeuLysGln 305
Db 1033 GAGAAATGGAGTTGCAACCGGATAGACACTTGACCCCGGTGTTTGTCTCGTCTAAACACAG 1092
QY 306 PheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLeuSer 325
Db 1093 TTTTCTGCAATGAATAAAATTAAGGAAGATGGCTTTAAAGGATGATAGCTGAGAGCCTCTCA 1152
QY 326 GluGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSerGly 345
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Qy 382 ThrIleAspTyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArgGlu 401
Db 1516 ACAATAGATTACAAAGAGTTTCATAGCTGCAACATTACATCTAAACAAATAGAGAGAG 1575
Qy 402 GluIleLeuValAlaPheSerAspPheAspLysAspGlySerGlyThrIleThrIle 421
Db 1576 GACCAATTGTTCGAGCTTTTACATACCTTTTGACAAAGATGGAGCGCTATATCACCCCA 1635
Qy 422 AspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMet 441
Db 1636 GACAGCTTCACACAGCTTGTGAGGATTTGGTGTTCAGGATGTCGCCATAGAGAACTG 1695
Qy 442 IleLysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAlaMet 461
Db 1696 ATCGCGCATGTTGATCAAGACAATGACGGCGCAATAGACTACAACGAGTTTGTGGCGATG 1755
Qy 462 MetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPheAsn 481
Db 1756 ATGCAGAAAGGAAGCATCACAGGAGGACCTGTGAAAAATGGTCTAGAGAAAAAGCTTTAGC 1815
Qy 482 IleAla 483
Db 1816 ATTGCT 1821

RESULT 9
US-09-828-313-26
; Sequence 26, Application US/09828313
; Patent No. US20020059662A1
; GENERAL INFORMATION:
; APPLICANT: COSTA e SILVA, OSWALDO DA
; APPLICANT: BOHNERT, HANS J.
; APPLICANT: THIELEN, NOCHA VAN
; APPLICANT: CHEN, ROUYING
; APPLICANT: SARRIA-MILLAN, RODRIGO
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; TITLE OF INVENTION: USE IN PLANTS
; FILE REFERENCE: 16313-0032
; CURRENT APPLICATION NUMBER: US/09/828,313
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/196,001
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 2230
; TYPE: DNA
; ORGANISM: Physcomitrella patens
US-09-828-313-26

Alignment Scores:
Pred. No.: 7.3e-163 Length: 2230
Score: 1509.50 Matches: 290
Percent Similarity: 75.47% Conservative: 70
Best Local Similarity: 60.80% Mismatches: 112
Query Match: 58.21% Indels: 5
DB: 9 Gaps: 3

US-09-848-806-1 (1-495) x US-09-828-313-26 (1-2230)

Qy 5 ProAsnProArgArgProSerAsnThr-----valLeuProTyrGlnThrProArg 21
Db 531 CCGAGCCGAGCCAGCATCGAGGTACGTATCCGGTGTTCGGGTAAAGCGCTGTGCAGAT 590
Qy 22 LeuArgAspHisTyrThrLeuLeuGlyLysLysLeuGlyGlnGlyGlnPheGlyThrThrTyr 41
Db 591 ATTTCGTCAATCTTACATCTCGGACGGGAGCTTGGCCGAGGCGAGTTCGAGTGACTTAC 650
Qy 42 LeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLys 61
Db 651 TTGTGTACTGACAAGATGCAATGAGGCGTACGGGTGCAAGAGCATGCCAAACGGAAA 710
Qy 62 LeuValCysArgGluAspTyrGluAspValTTPArgGluIleGlnIleMetHisLeu 81
```

```
Db 711 CTGACCAAGTAAGGAGGATATCGAGGATGTTAAGCGGAGGTTTCAGATTATGTCATCACCTG 770
Qy 82 SerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHis 101
Db 771 TCGGGGACACCCCAATATCGTGGTGTAAAGGATGTGTTCGAGGACAAGCATTCCTCGTCGAT 830
Qy 102 IleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHis 121
Db 831 CTTGTGATGAGCTCTGTGAGGTGGCGAGCTCTTCGATCGCATCATTCGCAAGGGCAT 890
Qy 122 PheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCys 141
Db 891 TACAGTGAGCGCGCCGCTGCGCATATCTGCAGAGTCATCTCATGTGTTGGTGCAGATGC 950
Qy 142 HisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerPro 161
Db 951 CACTCATATTAGGGTCTTCATCGGGATCTCAAGCCAGAGAATTTCTTGTGGCCAGCAAG 1010
Qy 162 LysAspAspAlaLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGly 181
Db 1011 GCTGAGATGCGCTCTGAAGGCCACAGACTTCGGTCTGTCAACTTTCTTTAAAGCCAGGA 1070
Qy 182 GlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLys 201
Db 1071 GATGTGTTCCAGGATATTGTTGAAGTGGCTATTACGTGGCCCTGAAGTTTGAAGAGA 1130
Qy 202 CysTyrGlyProGluIleAspValTTPSerAlaGlyValIleLeuTyrIleLeuLeuSer 221
Db 1131 AGTTATGGTCTCGAAGCTGATGTTGGAGTGCAGGCGTGTGTTGTATACATTCCTGCTGT 1190
Qy 222 GlyValProPheThrPalaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGly 241
Db 1191 GGTGTACCCCTTCTGGGCTGAACTGACGAGGATATCTTTGACGCTGTGCTCAAGGG 1250
Qy 242 LysLeuAspPheLysSerAspProTTPProThrIleSerGluAlaLysAspLeuIle 261
Db 1251 CACATAGACTTCGAGAACGATCCATGCCGAAATCTCCAACGGGGCTAAGGATTGGTG 1310
Qy 262 TyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGluAlaLeuCysHis 281
Db 1311 AGGAAATGCTAAACCTTAACGCTGAAGATACGCTCTGACGCGACAGCGGTGTGAACCAT 1370
Qy 282 ProTTPileValAspGluGlnAlaProAspLysProLeuAspProAlaValLeuSer 301
Db 1371 CATGATGAAGGAAGATGTTGATGCTCCAGAGTCCACTCGACAATTCGGGTGTGACC 1430
Qy 302 ArgLeuLysGlnPheSerGlnMetAsnLysIleLysMetAlaLeuArgValIleAla 321
Db 1431 AGACTGAAAAATTTCTCAGCCGCCAACAGATGAAAAAGCTGGCGCTGAAGGTGATTGCA 1490
Qy 322 GluArgLeuSerGluGluIleGlyGlyLeuLysGluLeuPheLysMetIleAspThr 341
Db 1491 GAGAGTCTGTCGAGGAGAGATCGTGGGTGTTGAGGAGATGTTCAATTCATAGATACA 1550
Qy 342 AspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValGlySer 361
Db 1551 GACAACAGCGGCACCGTGACGTTCGAGGAGCTTAAGGAAGGGTTCGTGAAGCGGGCTCA 1610
Qy 362 GluLeuMetGluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGly 381
Db 1611 AAATTAATGAATCGACATCAGAAACTAATGGAAGCTGCAGATGTCGATGGAAACGGC 1670
Qy 382 ThrIleAspTyrGlyGluPheLeuAlaThrLeuHisMetAsnLysMetGluArgGlu 401
Db 1671 AAGATCGACTTCAACAGAGTTTCAATCGGCAACAATGCAATGAAACAAAGCGGAAAGAG 1730
Qy 402 GluIleLeuValAlaPheSerAspPheAspLysAspGlySerGlyThrIleThrIle 421
Db 1731 GATCACCTTTGGCGAGCATTCATGCTATTCGACAGCAATAGCGGGTATATCACCATC 1790
Qy 422 AspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp---ThrProLeuAspAsp 440
```



Qy	206	GluileAspValtrpSerAlaGlyValIleLeuTyrlleLeuLeuSerGlyValProPro	225
Dd	709	GAGCTTGATATCGGACGTGGAGTTATCCTTTATATCCCTGCTGTGGTGTGCCACCA	768
Qy	226	PheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGlyLysLeuAspPhe	245
Dd	769	TTTTGGGCCGAGACTGAGCAAGGGGTGGCTCAGGCAGTCATTAGGTCAGTTATCGACTTT	828
Qy	246	LysSerAspProTrpThrIleSerGluAlaAlaLysAspLeuIleTyrlleLysMetLeu	265
Dd	829	AAGAGGGATCCATGGCCGAGAGTTTCTGACACTGCCAAGACCCTTGTGAGGAAGAATGCTC	888
Qy	266	GluArgSerProTylsLysArgIleSerAlaHisGluAlaLeuCysHisProTrpIleVal	285
Dd	889	GAACCTGACCCCAAAAAACGGCTTCTGCTGTCACAAGACTACTCGAACATCTCTTGGATACAA	948
Qy	286	AspGluGlnAlaAlaProAspLysProLeuAspProAlaValleuSerArgLeuLysGln	305
Dd	949	AATCGAAGGAAGGCTCCAAATGTTTCACTCGCGAGACGGTGAAGCAAGACTCAACACAG	1008
Qy	306	PheSerGlnMetAsnLysIleLysLysMetAlaLeuArgValIleAlaGluArgLeuSer	325
Dd	1009	TTTTCTGTTATGAACAGCTCAGAAAAGAGCCGTACGGGTGATAGCCGNAACACTTATCA	1068
Qy	326	GluGluGluLeuGlyLeuLysGluLeuPheLysMetIleAspThrAspAsnSergly	345
Dd	1069	GTGAGGAAGTAGCTGGCATCAAGGAAGCATTTGAGATGATGCACAGTAATAAAGACGGGA	1128
Qy	346	ThrIleThrPheGluGluLeuLysAlaGlyLeuLysArgValgly--SerGluLeuMet	364
Dd	1129	AAGATAAACCTCGAGGAGCTTAAATTTGGACTTTCATAAACTCGGACAGCAGACATACCT	1188
Qy	365	GluSerGluIleLysSerLeuMetAspAlaAlaAspIleAspAsnSerGlyThrIleAsp	384
Dd	1189	GATACTGATCTACAGATCTGATGGGAAGCTGCTGATGTTGATGGGATGGGACTTTAAAT	1248
Qy	385	TyrGlyGluPheLeuAlaAlaThrLeuHisMetAsnLysMetGluArgGluIleLeu	404
Dd	1249	TATGGGAGVTCTGGCTGTCTCTGTGCATCTTTAAGAAAAATGGCGAACGACGAACTTG	1308
Qy	405	ValAlaAlaPheSerAspPheAspLysAspGlySerGlyTyrlleThrIleaspGluLeu	424
Dd	1309	CATAAGGCTTTTAGCTTTTGTGACCAGATCAGAGCGATTTACATAGAGATTGAGGAGCTG	1368
Qy	425	GlnSerAlaCysThrGluPheGlyLeuCysAspThrProLeuAspAspMetIle----	442
Dd	1369	CGTGAGGCTTTAAATGAT-----GAGGTGGATACTAACAGTGAAGAAGTTGTTCAGCT	1422
Qy	443	-----LysGluIleAspLeuAspAsnAspGlyLysIleAspPheSerGluPheThrAla	460
Dd	1423	ATTATGCAAGATGTTGACACAGACAAGGACGGACGAATAAGCTATGAAGAGTTTGGCGCG	1482
Qy	461	MetMetArgLysGlyAspGlyValGlyArgSerArgThrMetMetLysAsnLeuAsnPhe	480
Dd	1483	ATGATGAAGCTGGAACAGATTGGAGGAAGCGTCGAGGCAATTTTCGCCGGAAAAATTC	1542
Qy	481	Asn 481	
Dd	1543	AAC 1545	

RESULT 12  
US-09-988-462-20  
; Sequence 20, Application US/09988462  
; Publication No. US20030046726A1  
; GENERAL INFORMATION:  
; APPLICANT: Koziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.  
; Warren, Gregory W.  
; Evola, Stephen V.  
; Greenleaf, Julian D.

Wright, Martha S.  
Merlin, Ellis J.  
Launig, Karen L.  
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
INSECTICIDAL ACTIVITY IN MAIZE

## NUMBER OF SEQUENCES: 94

## CORRESPONDENCE ADDRESS:

ADDRESSEE: Syngenta Biotechnology, Inc.  
STREET: 3054 Cornwallis Road  
CITY: Research Triangle Park  
STATE: NC  
COUNTRY: USA  
ZIP: 27709

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09/988,462

FILING DATE: 20-No. US20030046726A1-2001

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/547,422

FILING DATE: 11-APR-2000

APPLICATION NUMBER: US 08/459,504

FILING DATE: 02-JUN-1995

APPLICATION NUMBER: US 07/951,715

FILING DATE: 25-SEP-1992

APPLICATION NUMBER: US 07/772,027

FILING DATE: 04-OCT-1991

## ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: S-188051

## TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8587

TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 20:

## SEQUENCE CHARACTERISTICS:

LENGTH: 1349 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYPOTHETICAL: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 3..1226

OTHER INFORMATION: /note= "cDNA sequence for maize

pollen-specific calcium dependent protein kinase gene as

disclosed in Figure 30."

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-988-462-20

## Alignment Scores:

Pred. No.: 1.56e-136 Length: 1349  
Score: 1277.50 Matches: 242  
Percent Similarity: 76.98% Conservative: 59  
Best Local Similarity: 61.89% Mismatches: 89  
Query Match: 49.27% Indels: 1  
DB: 11 Gaps: 1

US-09-848-806-1 (1-495) x US-09-988-462-20 (1-1349)

Qy 76 GlnileMethHisLeuSerGluHisProAsnValValArgilleLysGlyThrTyGlu 95  
Db 3 CAGATCATGACCACTCTCCGGCCAGCCCAACGTGGTGGCCCTCCCGCGCGCGTACGAG 62  
Qy 96 AspSerValPheHisIleValMetGluValCysGluGlyGluLeuPheAspArg 115  
Db 63 GACAAGCAGAGCGTGCACCTCGTCATCGAGCTGTGCGCGCGCGGAGCTCTTCGACCGC 122

RESULT 13

Qy 116 IleValSerLysGlyHisPheSerGluArgGluAlaValLysLeuIleLysThrIleLeu 135  
Db 123 ATATCGCCCGCGGCGCATGACAGAGCGCGCGGAGCTCTCGCGCCATCGTG 182  
Qy 136 GlyValValGluAlaCysHisSerLeuGlyValMetHisArgAspLeuLysProGluAen 155  
Db 183 CAGATCGTGACACACTGCCACTCCATGGGGGTGATGCACCGGACATCAAGCCCGAGAAC 242  
Qy 156 PheLeuPheAspSerProLysAspAlaLysLeuLysAlaThrAspPheGlyLeuSer 175  
Db 243 TTCCTGTGCTCAGCAAGCAGAGCGCGCGCTCAAGGCGCACCGACTTCGGCTCTCC 302  
Qy 176 ValPheTyLysProGlyGlnTyLysPheValValGlySerProTyTyValAla 195  
Db 303 GTCTTCTCAAGGAGGCGGAGCTGCTCAGGACATCTCGCGGAGCGCTACTACATCGCG 362  
Qy 196 ProGluValLeuLysLysCysTyLysProGluIleAspValTrpSerAlaGlyValIle 215  
Db 363 CCCGAGGTGCTCAAGAGGAAGTACGCGCCGAGGCGGACATCTGGAGGCTCGGCGTCATG 422  
Qy 216 LeuTyLysLeuLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePhe 235  
Db 423 CTCTACATCTTCTCGCGGCGTGCCTCCTCTCTGGCAGAGAACGAGACGCGCATCTTC 482  
Qy 236 ArgGlnIleLeuGlnLysLeuAspPheLysSerAspProTrpProThrIleSerGlu 255  
Db 483 ACCGCCATCTCGGAGGCGAGCTTGACCTCTCCAGCGAGCATCGGCCACACATCTTCGCGG 542  
Qy 256 AlaAlaLysAspLeuIleTyLysMetLeuGluArgSerProLysLysArgIleSerAla 275  
Db 543 GGAGCCAGGATCTCGTCAAGAGATGCTCAACATCAACCCCAAGGAGCGGCTCAGCGG 602  
Qy 276 HisGluAlaLysCysHisProTrpIleValAspGluGlnAlaAlaProAspLysProLeu 295  
Db 603 TTCAGGTCTCTCAATCAATCCCATGGATCAAGAGAGAGGAGCGGCTGACACGCGCTT 662  
Qy 296 AspProAlaValLeuSerArgLeuLysGlnPheSerGlnMetAsnLysIleLysLysMet 315  
Db 663 GACAACGTTGTTCTCGACAGCTCAAGCAGTTCAGGCGCATGAACCATTTCAAGAAAGCA 722  
Qy 316 AlaLeuArgValIleAlaGluArgLeuSerGluGluIleGlyGlyLeuLysGluLeu 335  
Db 723 GCATTGAGGATCATAGCTGGGTGCCTATCCGAGAGGAGATCAAGGGCTGAGGAGATG 782  
Qy 336 PheLysMetIleAspThrAspAsnSerGlyThrIleThrPheGluGluLeuLysAlaGly 355  
Db 783 TTCAGAAACATTGACAAGGATAACAGCGGGAGCATTTACCTTCGACGAGCTCAAAACACGGG 842  
Qy 356 LeuLysArgValGlySerGluLeuMetGluSerGluIleLysSerLeuMetAspAlaAla 375  
Db 843 TTGCAAAAGCAGCGGCGCCAGCTGTGACAGAGCGAAATGGAGAACTAATCGAAGCAGCT 902  
Qy 376 AspIleAspAsnSerGlyThrIleAspTyxGlyGluPheLeuAlaAlaThrLeuHisMet 395  
Db 903 GACGCTCAGCGCAACGGGTTAATTGACTACGCGAATTCGTCACCGCAACAGTCATATG 962  
Qy 396 AsnLysMetGluArgGluGluIleLeuValAlaPheSerAspPheAspLysAspGly 415  
Db 963 AACAACTGGATAGAGAAGAGCACCTTTACACAGCATTTCCAGTATTTTCGACAGGACAA 1022  
Qy 416 SerGlyTyLysIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGlyLeuCysAsp 435  
Db 1023 AGCGGTACATTACTAAAGAGAGCTTGAGCAGCGCTTGAAGGAGCAAGGGTGTATGAC 1082  
Qy 436 Thr---ProLeuAspMetIleLysGluIleAspLeuAspAenAspGlyLysIleAsp 454  
Db 1083 GCGGATAAAATCAAGAGACATCATCTCCGATGCGGACTCTGACATGATGAGAGATAGAT 1142  
Qy 455 PheSerGluPheThrAlaMetMetArgLysGly 465  
Db 1143 TATTGAGGTTTGTGGCGATGATGAGGAAAGGG 1175

US-09-988-462-26  
; Sequence 26, Application US/09988462  
; Publication No. US20030046726A1  
; GENERAL INFORMATION:  
; APPLICANT: Kozziel, Michael G.  
; Desai, Nalini M.  
; Lewis, Kelly S.  
; Kramer, Vance C.  
; Warren, Gregory W.  
; Evola, Stephen V.  
; Crossland, Lyle D.  
; Wright, Martha S.  
; Merlin, Ellis J.  
; Launis, Karen L.  
; TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED  
; INSECTICIDAL ACTIVITY IN MAIZE  
; NUMBER OF SEQUENCES: 94  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Syngenta Biotechnology, Inc.  
; STREET: 3054 Cornwalis Road  
; CITY: Research Triangle Park  
; STATE: NC  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/988,462  
; FILING DATE: 20-No. US20030046726A1-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 09/547,422  
; FILING DATE: 11-APR-2000  
; APPLICATION NUMBER: US 08/459,504  
; FILING DATE: 02-JUN-1995  
; APPLICATION NUMBER: US 07/951,715  
; FILING DATE: 25-SEP-1992  
; APPLICATION NUMBER: US 07/772,027  
; FILING DATE: 04-OCT-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: S-188051  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919)541-8587  
; TELEFAX: (919)541-8689  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4162 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 1418..1427  
; OTHER INFORMATION: /note= "start of mRNA"  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 1481..2366  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 2367..2451  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 2452..2602  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 2603..2690  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 2691..2804  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 2805..2906  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 2907..3075  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 3076..3177  
; FEATURE:  
; NAME/KEY: exon  
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; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 3305..3398  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 3399..3498  
; FEATURE:  
; NAME/KEY: intron  
; LOCATION: 3499..3713  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: 3714..3811  
; SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-988-462-26  
Alignment Scores:  
Pred. No.: 2,96e-122 Length: 4162  
Score: 1159.50 Matches: 276  
Percent Similarity: 50.00% Conservative: 69  
Best Local Similarity: 40.00% Mismatches: 115  
Query Match: 44.72% Indels: 235  
DB: 11 Gaps: 7  
US-09-848-806-1 (1-495) x US-09-988-462-26 (1-4162)  
QY 6 AsnProArgProSerAsnThrValLeuProTyrGlnThrProArgLeuArgAspHis 25  
Db 1698 AACCGCGCGCGCGGTG-GGCACGGTGTGGCGGCCCATGGAGGACGTGGCGCGGACC 1756  
QY 26 TyrLeuLeuGlyLysLysLeuGlyGlnGlnPheGlyThrThrTyrLeuCysThrGlu 45  
Db 1757 TACTCGATGGCAAGAGCTCGGGCGCGGCGATTCTCGCGTGCACCATCTGTGCACGCAC 1816  
QY 46 LysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLysLeuValCysArg 65  
Db 1817 CGGACGAGCGCGGAGAGCTGGCGTGCAGACGATCGCGAAGCGGAGCTGGCGCGGACG 1876  
QY 66 GluAspTyrGluAspValTrpArgGluIleGlnIleMetHisLeuSerGluHisPro 85  
Db 1877 GAGGACGTGGACGACGTGGCGGGAGGTGCAGATCATGCACCATCTCTCGGCGCAGCCC 1936  
QY 86 AsnValValArgIleLysGlyThrTyrGluAspSerValPheValHisIleValMetGlu 105  
Db 1937 AACGTGGTGGGCTTCGGCGCGCGTACGAGGCAAGACGAGCGTGCACCTCGTCATGGAG 1996  
QY 106 ValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHisPheSerGluArg 125  
Db 1997 CTGTGGCGGGGGGAGGCTCTTCACCGCATCATCGCCGGGGCCAGTACACGGAGCGC 2056  
QY 126 GluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCysHisSerLeuGly 145  
Db 2057 GCGCGCGCGGAGCTGTGGCGCCCATCGTGACGCGTGCACACCATCTGCCATCTCATGGG 2116  
QY 146 ValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerProLysAspAla 165  
Db 2117 GTGATGCACCGGGACATCAAGCCCGAGAACTTCTCTGCTCTCAGCAAGACGAGGACGG 2176  
QY 166 LysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGlyGlnTyrLeuTyr 185





Qy	5	ProAsnProArgArgProSerAsnThr-----ValLeuProTyrGlnThrProArg	21
Db	579	CCGAGGCGCAAGCAGCATCCAGGTACGTATCCGGTGTTTTGGTAAAGCCGCTGCAGAT	638
Qy	22	LeuArgAspHisTyrLeuLeuGlyLysLeuGlyGlnGlyGlnPheGlyThrTyr	41
Db	639	ATTGGTCAATCTTACATCTCGGACGGGAGCTTGGCCGAGGGCAGTTCGGAGTCACTTAC	698
Qy	42	LeuCysThrGluLysSerThrSerAlaAsnTyrAlaCysLysSerIleProLysArgLys	61
Db	699	TTGTGTACTGACAAAGATGACCAATGACGGCGTACGCGTCAAGAGCATCCGCAACGGAAA	758
Qy	62	LeuValCysArgGluAspTyrGluAspValTrpArgGluIleGlnIleMetHisIle	81
Db	759	CTGACCTAGTAGGAGGATATCGAGATGTTAAGCGGGAGGTTCAGATTATGATCATCACCCTG	818
Qy	82	SerGluHisProAsnValValArgIleLysGlyThrTyrGluAspSerValPheValHis	101
Db	819	TCGGGGACACCCAATATCGTGGTGTAAAGGATGTTCTCGAGGACACAGCATTCGTCGCAT	878
Qy	102	IleValMetGluValCysGluGlyGlyGluLeuPheAspArgIleValSerLysGlyHis	121
Db	879	CTTGTGATGGAGCTCTGTGCAGGTGGCAGGCTCTTCGATCGATCATTCATGCCAAGGGCAT	938
Qy	122	PheSerGluArgGluAlaValLysLeuIleLysThrIleLeuGlyValValGluAlaCys	141
Db	939	TACAGTGAAGCCGCGCTGCCGATATGTGCAGAGTCATGTCGAATGTGGTGACACAGATGC	998
Qy	142	HisSerLeuGlyValMetHisArgAspLeuLysProGluAsnPheLeuPheAspSerPro	161
Db	999	CACTCATTAGGGGTCTTCCATCGGGATCTCAAGCCACAGAAATTTCTGTGGCCAGCAG	1058
Qy	162	LysAspAlaLysLysLeuLysAlaThrAspPheGlyLeuSerValPheTyrLysProGly	181
Db	1059	GCTGAGATGCGCTCTGTAAGGCCACACAGACTTCGGTCTGTCAACTTCTTTAAGCCAGGA	1118
Qy	182	GlnTyrLeuTyrAspValValGlySerProTyrTyrValAlaProGluValLeuLysLys	201
Db	1119	GATGTGTTCCAGGATATGTGTGAAGTGCCTGATTACGTGGCCCTGAAGTTTGAAGAGA	1178
Qy	202	CysTyrGlyProGluIleAspValTrpSerAlaGlyValIleLeuTyrIleLeuLeuSer	221
Db	1179	AGTTATGGTCTCGAGCT-GATGTTTGAGTGCAGCGCTGATGTGGTACATTCGTCGTGT	1237
Qy	222	GlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGlnIleLeuGlnGly	241
Db	1238	GGTGATACCCCTTCTCGGCTGAAACTGACAGGGGTATCTTTGACGCTGTGCTCAAAAGG	1297
Qy	242	LysLeuAspPheLysSerAsp-ProTrpProThrIleSerGluAlaLysAspLeuIle	261
Db	1298	CACATAGACTTCGAGACGAGTCCATGCGCGAAAATCTCCAACGGGGCTAAGGATTGGT	1357
Qy	261	eTyrLysMetLeu	265
Db	1358	GAGGAAAATGCTA	1370

RESULT 15

US-09-828-313-25

Sequence 25, Application US/09828313  
Patent No. US20020059662A1  
GENERAL INFORMATION:  
APPLICANT: COSTA e SILVA, OSWALDO DA  
APPLICANT: BOHNERT, HANS J.  
APPLICANT: THIELEN, NOCHA VAN  
APPLICANT: CHEN, ROUYING  
APPLICANT: SARRIA-MILLAN, RODRIGO  
TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF  
TITLE OF INVENTION: USE IN PLANTS  
FILE REFERENCE: 16313-0032  
CURRENT APPLICATION NUMBER: US/09/828,313  
CURRENT FILING DATE: 2001-04-06  
PRIOR APPLICATION NUMBER: 60/196,001  
PRIOR FILING DATE: 2000-04-07



```
Qy 218 IleLeuLeuSerGlyValProPheTrpAlaGluThrGluSerGlyIlePheArgGln 237
Db |||||
1050 ATTTTGTATGTGTAGTCGACCGTTTGGCGCGGACCGAGTCGGGCATTTTCGTGCG 1109
Qy 238 IleLeuGlnGlyLysLeuAspPheLysSerProTrpProThrIleSerGluAla 257
Db |||||
1110 GTGTTGAGGGGTGACCCGAGCTTTGAAGAAGCCCTTGGCCCTCCATCTCTCCGAAGCC 1169
Qy 258 LysAspLeuIleTyrLysMetLeuGluArgSerProLysLysArgIleSerAlaHisGlu 277
Db |||||
1170 AAGGATTCGTGAAGCTCTCTGTAATAGGATATGCCGAACCGCATGCTGCTGCACAA 1229
Qy 278 AlaLeuCysHisProTrpIleValAspGluGlnAlaAlaProAspLysProLeuAspPro 297
Db |||||
1230 GCTTTAACTCATCCATGATTCGAAGTAACAACGTG-----AAGATACCTCTGGATATC 1283
Qy 298 AlaValLeuSerArgLysGlnPheSerGlnMetAsnLysIleLysLysMetAlaLeu 317
Db |||||
1284 TTAGTGTAACAGCTGTGAGGAATTCCTCGTCATCATCCATGAGAAAGGCTGCTTTG 1343
Qy 318 ArgValIleAlaGluArgLysSerGluGluIleGlyLysGluLysGluLeuPheLys 337
Db |||||
1344 AAGGCCCTGTCAAGACTTTTAACCGAAGACGAGACTTTTATCTACGTACTCAATTTATG 1403
Qy 338 MetIleAspThrAspAsnSerGlyThrIlePheGluGluLeuLysAlaGlyLeuLys 357
Db |||||
1404 CTGTAGAACCAAGTAACAACGGTCTGTACTTTTGAGAAATTTTCAGACAGGCACCTGCTG 1463
Qy 358 ArgValGlySerGluLeuMet--GluSerGluIleLysSerLeuMetAspAlaAlaAsp 376
Db |||||
1464 AAAAATTCACAGAGGCCATGAAAGAGTCACGGGTTTTTGAAATTCGAAATCGATGGAT 1523
Qy 377 IleAspAsnSerGlyThrIleAspTyrGlyPheLeuAlaAlaThrLeuHisMetAsn 396
Db |||||
1524 GGTCTTCATTTCAAGAAATGGACTTTTCAGAGTTCTGTGCGCGGCCATTAGTGTCTC 1583
Qy 397 LysMetGluArg-----GluIleLeuValAlaAlaPheSerAspPheAsp 412
Db |||||
1584 CAGTTAGAAGCCACAGAACGATGGGAGCAGCATGCTCGCGCAGCTTACGACATATTGAG 1643
Qy 413 LysAspGlySerGlyTyrIleThrIleAspGluLeuGlnSerAlaCysThrGluPheGly 432
Db |||||
1644 AAAGAGGTACCGAGTCATTTCCTGATGAACCTT-----GCGAAGAGATGGGA 1694
Qy 433 LeuCys---AspThrProLeuAsp-----AspMetIleLysGluIleAspLeuAsp 448
Db |||||
1695 CTAGCACCAAATGTACCAGCCCAAGTGTTCCTAGATTGGATTAGACAG----- 1742
Qy 449 AsnAspGlyLysIleAspPheSerGluPheThrAlaMetMetArgLysGlyAspGlyVal 468
Db |||||
1743 TCTGATGGTCGGGTGAGTTTCACCTGGGTTTCCACCAAGCTGTACAT----- 1787
Qy 469 GlyArgSerArgThrMetMetLysAsnLeu 478
Db |||||
1788 GGAATTTCCAGCCGTGTATCAAAAATCTC 1817
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Job time : 1208 secs